STIC-Biotech/ChemLib

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Hutzell, Paula

Sent:

Monday, March 29, 2004 8:30 AM

To:

Holleran, Anne; STIC-Biotech/ChemLib Chan, Christina

Cc: Subject:

RE: RUSH sequence search for 09/477,082

approved

----Original Message---

From:

Holleran, Anne

Sent:

Friday, March 26, 2004 12:02 PM

To:

Hutzell, Paula

Cc:

Chan, Christina

Subject:

FW: RUSH sequence search for 09/477,082

----Original Message----

From:

Holleran, Anne

Sent:

Friday, March 26, 2004 12:01 PM

To:

Chan, Christina

Subject:

RUSH sequence search for 09/477,082

Please approve and forward to STIC the following RUSH sequence search request. This is for an amendment due this biweek. Thanks.

Please search the following for 09/477,082

interference databases only search of SEQ ID NO: 1(na) interference databases only search of SEQ ID NO: 2(na)

commercial and interference database search of SEQ ID NO: 29, 30, 31, 32, 33, 34(na), these are primer sequences Please perform a Score/Length sequence search for the primer sequences (SEQ ID NO: 29-34) with a minimum hit length of 15 and a maximum hit length of 40, and a score over length value of 90% or greater

SEQ ID NO: 1 and SEQ ID NO: 2 are two different regions of the same gene

Anne Holleran

AU: 1642

Tel: (571) 272-0833 RM: Remsen, 3A14

mailbox: Remsen, 3C18

Searcher: Location: Date Picked Up: Date Completed: 3/3 Searcher Prep/Review: Clerical: Online time:

TYPE OF SEARCH: NA Sequences:_ AA Sequences:_ Structures: Bibliographic:_ Litigation:_ Full text: Patent Family:

Other:_

VENDOR/COST (where applic.) STN: DIALOG: Questel/Orbit: DRLink: Lexis/Nexis: Sequence Sys.: WWW/Internet: Other (specify):

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5313	13.4	. 2	15	6	AR208417	0.893333
c5314	13.4	2	15	6	AX802132	0.893333
5315	13.4	2	15	6	BD208917	0.893333
8164	13	1.9	15	6	AX009449	0.866667
c1846	14.4	2.1	17	6	AX758412	0.847059
1847	14.4	2.1	17	8	ATH52680	9 0.847059
1848	14.4	2.1	17		ATH52681	
5316	13.4	2	16		AR080878	0.8375
c5317	13.4	2	16		BD266396	0.8375
c5318	13.4	2	16		BD104574	0.8375
1082	15	2.2	18		AX378655	0.833333
15795	12.4	1.9	15		A52100	0.826667
15796	12.4	1.9	15	1	A52101	0.826667
15797	12.4	1.9	15		A52128	0.826667
15798	12.4	1.9	15		A52129	0.826667
15799	12.4	1.9	15		A65237	0.826667
15800	12.4	1.9	15		A66708	0.826667
15801	12.4	1.9	15		A66711	0.826667
15802	12.4	1.9	15		A68206	0.826667
15802		1.9	15		A68260	0.826667
10003	12.4	1.9	13		700200	0.020007

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7279	13.4	2	15	3	AAZ64339	0.89333
c7280	13.4	2	15		AAH74112	0.89333
7281	13.4	2	15		AAD39760	0.89333
7282	13.4	2	15		ABX01392	0.89333
11340	13	1.9	15		AAZ48115	0.86666
c2401	14.4	2.1	17		ABN07749	0.84705
c2402	14.4	2.1	17		ABN07750	0.84705
c2403	14.4	2.1	17		ADB41410	0.84705
c17300	12.6	1.9	15		ABA03942	0.04703
c7283	13.4	2	16		ABL31189	0.837
1374	15.4	2.2	18		ABK41196	0.83333
21562	12.4	1.9	15		AAQ29530	0.82666
		1.9	15			0.82666
21563	12.4	1.9	15	2		0.82666
21564	12.4		15		AAT31819	0.82666
21565	12.4	1.9				
c21566	12.4	1.9	15		AAX64708	0.82666
21567	12.4	1.9	15		AAT50054	0.82666
c21568	12.4	1.9	15		AAT50251	0.82666
21569	12.4	1.9	15		AAV07762	0.82666
21570	12.4	1.9	15		AAV07759	0.82666
21571	12.4	1.9	15		AAV06230	0.82666
21572	12.4	1.9	15		AAX33998	0.82666
21573	12.4	1.9	15		AAV06801	0.82666
21574	12.4	1.9	15		AAV48551	0.82666
21575	12.4	1.9	15		AAV06817	0.82666
21576	12.4	1.9	15	3	AAZ64338	0.82666
21577	12.4	1.9	15	3	AAA07813	0.82666
21578	12.4	1.9	15	4	AAH20310	0.82666
21579	12.4	1.9	15	4	AAF31459	0.82666
21580	12.4	1.9	15	4	AAF59902	0.82666
21581	12.4	1.9	15	4	AAF59905	0.82666
21582	12.4	1.9	15	4	AAF31566	0.82666
21583	12.4	1.9	15	4	AAF52237	0.82666
c21584	12.4	1.9	15	4	AAF52606	0.82666
21585	12.4	1.9	15	4	AAF52236	0.82666
c21586	12.4	1.9	15	4	AAF52607	0.82666
21587	12.4	1.9	15		AAH28548	0.82666
21588	12.4	1.9	15	4	AAF97971	0.82666
c21589	12.4	1.9	15		AAD41857	0.82666
21590	12.4	1.9	15		ABX01391	0.82666
21591	12.4	1.9	15		ABK98173	0.82666
21592	12.4	1.9	15		ABK98172	0.82666
21593	12.4	1.9	15		ABK98144	0.82666
21594	12.4	1.9	15		ABX16342	0.82666
21595	12.4	1.9	15		ADC66181	0.82666
21596	12.4	1.9	15		ADC66180	0.82666
c3721	14	2.1	17		ABT40012	0.82352
c3721	14	2.1	17		ADE25256	0.82352
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c9066	12.4	1.9	15	1	US-07-799-824-4	0.826667
c9067	12.4	1.9	15		US-07-976-103A-4	0.826667
c9068	12.4	1.9	15		US-08-363-240A-665	0.826667
9069	12.4	1.9	15		US-08-426-807-1	0.826667
9070	12.4	1.9	15		US-08-311-486C-16	0.826667
c9071	12.4	1.9	15		US-07-892-902-6	0.826667
9072	12.4	1.9	15		US-07-892-902-7	0.826667
c9073	12.4	1.9	15		US-08-473-481-4	0.826667
c9073	12.4	1.9	15		US-08-585-684B-202	0.826667
9075	12.4	1.9	15		US-08-459-434-1	0.826667
c9076	12.4	1.9	15		US-09-038-073-202	0.826667
c9076	12.4	1.9	15		US-08-338-352-5	
						0.826667
9078	12.4	1.9	15		US-09-202-294-1	0.826667
c9079	12.4	1.9	15		US-08-599-738A-4	0.826667
9080	12.4	1.9	15		US-09-612-531-4	0.826667
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9092	12.4	1.9	15	4	US-09-612-531-22	0.826667
9093	12.4	1.9	15	4	US-09-612-531-23	0.826667
9094	12.4	1.9	15	4	US-09-612-531-24	0.826667
9095	12.4	1.9	15	4	US-09-612-531-25	0.826667
9096	12.4	1.9	15	4	US-09-142-212A-3	0.826667
9097	12.4	1.9	15	4	US-09-142-212A-4	0.826667
9098	12.4	1.9	15	4	US-09-142-212A-5	0.826667
9099	12.4	1.9	. 15	4	US-09-142-212A-6	0.826667
9100	12.4	1.9	15		US-09-142-212A-9	0.826667
9101	12.4	1.9	15		US-09-142-212A-13	0.826667
9102	12.4	1.9	15	-	US-09-349-040A-6	0.826667
9103	12.4	1.9	15		US-09-349-040A-7	0.826667
9104	12.4	1.9	15		US-09-349-040A-8	0.826667
9105	12.4	1.9	15		US-09-753-943D-3	0.826667
9106	12.4	1.9	15		US-09-753-943D-4	0.826667
9107	12.4	1.9	15		US-09-753-943D-6	0.826667
9108	12.4	1.9	15		US-09-753-943D-7	0.826667
9109	12.4	1.9	15		US-09-753-943D-8	0.826667
9110	12.4	1.9	15		US-09-753-943D-9	0.826667
c9111	12.4	1.9	15		US-09-753-943D-10	0.826667
c9112		1.9	15		US-09-753-943D-10	
c9112	12.4	1.9			US-09-753-943D-11	0.826667
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Result		Query				
No.	Score	Match	Length	DB	ID	S/L
4092	13.4	2			US-09-504-231A-1174	0.893333
4093	13.4	2			US-09-274-553D-1174	0.893333
c1318	14.4	2.1	17	9	US-09-866-108-7741	0.847059
c1319	14.4	2.1	17	9	US-09-866-108-7742	0.847059
1320	14.4	2.1	17		US-09-730-289B-27	0.847059
c1321	14.4	2.1	17		US-10-230-006-50	0.847059
c1322	14.4	2.1	17	14	US-10-230-006-547	0.847059
1323	14.4	2.1	17	15	US-10-300-683-252	0.847059
c4094	13.4	2	16		US-10-297-068-678	0.8375
690	15	2.2	18	12	US-10-333-429-444	0.833333
12708	12.4	1.9	15		US-09-504-231A-1173	0.826667
12709	12.4	1.9	15		US-09-274-553D-1173	0.826667
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12711	12.4	1.9	15	14	US-10-247-893-8	0.826667
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c2513	13.8	2.1	17		US-09-866-108-9786	0.811765
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c2519	13.8	2.1	17		US-09-817-879-1246	0.811765
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Result	0.4.1.1		Length	DB	ID	S/L
Result No.	Score	Match				1
No.				7-	110 40 000 000	<u> </u>
No. c 667	17	2.5			US-10-293-338-3956	1
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	14.4					0.84705
c16444	14.4	2.1	17	32	US-10-471-271-4734	0.84705

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model March 29, 2004, 16:45:00; Search time 101.23 Seconds Run on: (without alignments) 4020.727 Million cell updates/sec US-09-477-082-1 Title: Perfect score: 670 Sequence: 1 aagcgctccaagacacgatt.....ggggttaaataaagcgcttt 670 Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0 1268986 segs, 303744313 residues Searched: 956702 Total number of hits satisfying chosen parameters: Minimum DB seq length: 15 Maximum DB seq length: 40 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 65000 summaries Pending_Patents_NA_New:* Database: 1: /cgn2 6/ptodata/1/pna/PCT_NEW_COMB.seq:* 2: /cgn2 6/ptodata/1/pna/US06_NEW_COMB.seq:* 3: /cgn2 6/ptodata/1/pna/US07 NEW COMB.seg:* 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:* 5: /cgn2 6/ptodata/1/pna/US09 NEW COMB.seq:* 6: /cgn2 6/ptodata/1/pna/US10_NEW_COMB.seq:* 7: /cgn2 6/ptodata/1/pna/US60 NEW_COMB.seq:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. **SUMMARIES** % Result Query S/L DB ID Match Length No. Score 6 US-10-607-077A-43 0.8 4525 12.8 1.9 16 0.8 6 US-10-708-204-5066 c4526 12.8 1.9 16 0.79 1 PCT-US04-04452-1157 c 58 15.8 2.4 20 2.2 19 5 US-09-646-399A-3 0.789474 203 15

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16467	11.8	1.8	15	6	US-10-045-674A-622	0.786667
16468	11.8	1.8	15	6	US-10-785-116-5	0.786667
169	15.2	2.3	20	6	US-10-780-439-41	0.76
170	15.2	2.3	20	6	US-10-690-276-106	0.76
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4527	12.8	1.9	17		PCT-US03-27118-12	0.752941
59	15.8	2.4	21		PCT-US04-00035-9257	0.752381
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7644	12.4	1.9	17		US-09-941-492A-16	0.729412
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c1148	13.8	2.1	19		US-10-664-668-469	0.726316
1149	13.8	2.1	19		US-10-665-951-42	0.726316
c1150	13.8	2.1	19	· · · · · · · · · · · · · · · · · · ·	US-10-665-951-469	0.726316
c1151	13.8	2.1	19		US-10-444-925A-309	0.726316
c 172	15.2	2.3	21		PCT-US04-00035-17210	0.72381
c52331	10.8	1.6	15		PCT-US04-07220-7	0.72381
c52332	10.8	1.6	15		US-10-792-374-28	0.72
2	17.8	2.7	25		US-60-545-213-161396	0.72
c4528	12.8	1.9	18		US-10-021-698A-6079	
c 708	14.2	2.1	20			0.711111
c12939	14.2	1.8	17		US-09-970-851-5	0.71
12940	12				PCT-US03-31862-879	0.705882
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c 294	14.8	2.2	21		PCT-US04-00035-17209	0.704762
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c 298	14.8	2.2	21		US-10-770-726-7109	0.704762
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32789	11.2	1.7	16		US-10-796-280-68262	0.7
c 354	14.6	2.2	21		PCT-US04-00035-8051	0.695238
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360	14.6	2.2	21		US-10-770-726-18917	0.695238
361	14.6	2.2	21	6	US-10-770-726-18918	0.695238

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OM nucleic - nucleic search, usir	ng sw model			
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Title: US-09-477-082-1				
Perfect score: 670				
Sequence: 1 aagcgctccaagac	cacgatt	ggggttaaa	taaagcgcttt	670
Scoring table: IDENTITY_NUC				
Gapop 10.0 , Gapext 1	1.0			
Searched: 27513289 seqs, 1	4931090276	residues		
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	29: gb_gss2					
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Result		Query				
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7147	11.8	1.8	15		BQ590656	0.786667
7148	11.8	1.8	15		BQ591170	0.786667
7149	11.8	1.8	15		BQ591178	0.786667
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7151	11.8	1.8	15		BQ594689	0.786667
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7154	11.8	1.8	15		CF290920	0.786667
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7157	11.8	1.8	15		CF291717	0.786667
7158	11.8	1.8	15		CF291798	0.786667
7159	11.8	1.8	15		CF292458	0.786667
7160	11.8	1.8	15		CF292461	0.786667
7161	11.8	1.8	15		CF298148	0.786667
7162	11.8	1.8	15		CF298630	0.786667
7163	11.8	1.8	15		CF298733	0.786667
7164	11.8	1.8	15		CF298805	0.786667
7165	11.8	1.8	15		CF298889	0.786667
7166	11.8	1.8	15		CF299602	0.786667
7167	11.8	1.8	15		CF299608	0.786667
7168	11.8	1.8	15		CF300121	0.786667
7169	11.8	1.8	15		CF300361	0.786667
7170	11.8	1.8	15		CF300992	0.786667
7171	11.8	1.8	15		CF302034	0.786667
7172	11.8	1.8	15		CF302124	0.786667
7173	11.8	1.8	15		CF302182	0.786667
7174	11.8	1.8	15		CF307923	0.786667
			.0	17	J. 33.323	55557

	Co	nCore versi	on 5 1 6			
			001 3.1.0 2004 Comp	ugen I td	-	
	Copyright	(6) 1990 - 2	.004 Comp	ugen Eta.		
OM nucleio	c - nucleic s	earch, usin	g sw model			
Run on:	March 2	9, 2004, 12	:49:34 ; Sea	arch time 3	004.06 Seco	nds
		(with	out alignmei	nts)		
		10864	4.389 Millio	n cell upda	tes/sec	
Title:	US-09-477	-082-2				
Perfect sco		<u></u>				
Sequence:	1 aatta	gaccgcgtat	tgaaa	.tacactggttt	tttaacctt 753	
Caarina tak	No. IDENT	ITY NILIC				
	ole: IDENT Gapop 10.0		0			
	зарор то.о	, Gapexi i	.0			
Searched:	347027	2 seas 216	 71516995	residues		
Journal of tou.	347027	_ 00q0, _ 10		J014403		
Total numb	er of hits s	atisfying ch	osen param	eters: 1	364278	
		, , , , , ,				
Minimum E	B seq leng	th: 15				
Maximum	DB seq lenç	gth: 40				
	ssing: Minir					
	Maximum I					
	Listing first	65000 sum	maries			
Databasa :	GenEn	abl:*				
Database :	Gen⊵n l: gb_ba:*	IIDI."				
	2: gb_ba. 2: gb_htg:*					
	3: gb_in:*					
	1: gb_om:*					
	5: gb_ov:*					
	3: gb_pat:*					
	7: gb_ph:*					
8	3: gb_pl:*					
(9: gb_pr:*					
1	10: gb_ro:*					
	<pre>11: gb_sts:</pre>					
	12: gb_sy:*					
	13: gb_un:*					
	l4: gb_vi:*					
	15: em_ba:					
	l6: em_fun l7: em_hur					
	17. em_nur 18: em_in:*					
	19: em_mu					
	20: em_om				-	
	21: em_or:					
	22: em_ov:				-	
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	10	•				
	3: em_pat					
	4: em_ph:			·		
	5: em_pl:*					
l	:6: em_ro:*					
	?7: em_sts:					
	.8: em_un:					
	9: em_vi:*					
	0: em_htg					
3	1: em_htg	_inv:*				
3	2: em_htg	_other:*				
3	3: em_htg	_mus:*				
3	4: em_htg	_pln:*				
3	5: em_htg	_rod:*				
3	6: em_htg	_mam:*				
	7: em_htg					
	8: em sy:					
	9: em_htg					
4	0: em_htg	o mus:*				
	1: em_htg					
	// J			<u> </u>		
Pred N	lo is the nu	mber of res	sults predict	ed by chan	ce to have a	1
					being printe	
			he total sco			
4,14,15	ionited by e	inalyolo or i	line total ood			
ļ		SUMMAR	IFS			
		%				
Result		Query				
No.	Score	Match	Length	DB	ID	S/L
4757	14	1.9	15	6	AR231294	0.933333
c3023	14.4	1.9	16		A36563	0.9
3024	14.4	1.9	16		AR002257	0.9
3025	14.4	1.9	16		AR045207	0.9
3026	14.4	1.9	16		AR051238	0.9
c3027	14.4	1.9	16		AR087164	0.9
c3028	14.4	1.9	16		AR150597	0.9
c3029	14.4	1.9	16		E36063	0.9
3030	14.4	1.9	16		116032	0.9
3031	14.4	1.9	16		128367	0.9
c3032	14.4	1.9	16		142181	0.9
c3032	14.4	1.9	16		142187	0.9
	14.4	1.9	16		149619	0.9
c3034					L	
c3035	14.4	1.9	16		AR200478	0.9
c3036	14.4	1.9	16		AR371265	0.9
8238	13.4	1.8	15		AR029856	0.893333
c8239	13.4	1.8	15		AR029872	0.893333
8240	13.4	1.8	15		AR056159	0.893333
8241	13.4	1.8	15	6	AR056160	0.893333

	Gal	nCore version	n 5 1 6			
		(c) 1993 - 20		igen I td		
	Copyright	(6) 1993 - 20	004 Comp	agen Ltd.		
014						
OM nucleio	c - nucleic s	earch, using	sw model			
					5 400 0	
Run on:	March 2				5.436 Secon	ias
			ut alignmer			
		9829.	571 Million	cell updates	s/sec	
Title:	US-09-477	'-082-2				
Perfect sco						
Sequence:	1 aatta	gaccgcgtatt	gaaa	tacactggtttt	ttaacctt 753	
		·				
Scoring tal	ole: IDENT	ITY_NUC				
	Gapop 10.0	, Gapext 1.	0			
Searched:	337386	3 seqs, 212	4099041 re	sidues		
000.0						
Total numb	ner of hits s	atisfying cho	sen naram	eters: 20	72792	
Total Haili	1	unsiying on	soon param			
Minimum I	DB seq leng	th: 15				
	DB seq leng					
Maximum	DB sed leni	giri. 40				
			00/			
Post-proce	ssing: Minii	mum Match	0%			
		Match 100%				
	Listing first	65000 sum	maries		· · · · · · · · · · · · · · · · · · ·	
Database:		neseq_29Ja	n04:*			
	1: geneseq					
	2: geneseq					
	3: genesed					
	4: genesed	n2001as:*				
	5: geneseq	n2001bs:*				
	6: genesed					
	7: genesed	n2003as:*				
	8: genesed					
	9: genesed					
	10: genese					
<u> </u>	. J. gonose	7				
Pred I	Vo is the n	umber of res	sults predic	ted by chan	ce to have a	
					being printe	
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and is	delived by	analysis Ul t	ווס נטנמו שנו	JIG GISHIDUH	OII.	
	J	CLIBARAAD	IEC			
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<u> </u>		%				
Result		Query			15	0.0
No.	Score	Match	Length	DB	ID	S/L
						-
6			21		AAA51822	1
c 7	21	2.8	21	3	AAA51823	1

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120	18	2.4	20		ADE43355	0.9
3730	14.4	1.9	16		AAQ20008	0.9
3731	14.4	1.9	16		AAX18362	0.9
10799	13.4	1.8	15	2	AAQ21631	0.893333
10800	13.4	1.8	15	2		0.893333
10801	13.4	1.8	15	2	AAT52140	0.893333
10802	13.4	1.8	15	2	AAT52142	0.893333
10803	13.4	1.8	15	2	AAX14658	0.893333
c10804	13.4	1.8	15	2	AAX14674	0.893333
10805	13.4	1.8	15	5	AAA91455	0.893333
10806	13.4	1.8	15	5		0.893333
c10807	13.4	1.8	15	6		0.893333
10808	13.4	1.8	15	6	ABK81789	0.893333
c10809	13.4	1.8	15	7	ABZ66579	0.893333
c2080	15	2	17	9	ADE25221	0.882353
5799	14	1.9	16	2	AAX61143	0.875
15897	13	1.7	15	3	AAZ59262	0.866667
15898	13	1.7	15	4	AAF81549	0.866667
15899	13	1.7	15	4	AAF49044	0.866667
15900	13	1.7	15	4	AAF49043	0.866667
15901	13	1.7	15	4	AAF49042	0.866667
15902	13	1.7	15	5	AAH23587	0.866667
15903	13	1.7	15	6	ABA97405	0.866667
c15904	13	1.7	15	6	ABK72352	0.866667
15905	13	1.7	15	6	ABK98166	0.866667
15906	13	1.7	15	6	ABK98185	0.866667
15907	13	1.7	15	7	AAD47757	0.866667
15908	13	1.7	15	8	ADB68522	0.866667
8868	13.6	1.8	16	4	AAF82119	0.85
8869	13.6	1.8	16	5	AAH27758	0.85
8870	13.6	1.8	16	6	AAD44149	0.85
126	17.8	2.4	21	3	AAA51818	0.847619
3732	14.4	1.9	17	2	AAQ20006	0.847059
3733	14.4	1.9	17	2	AAQ20005	0.847059
3734	14.4	1.9	17	2	AAX69798	0.847059
3735	14.4	1.9	17	2	AAX69799	0.847059
3736	14.4	1.9	17		AAS06654	0.847059
c3737	14.4	1.9	17		ACC51390	0.847059
c3738	14.4	1.9	17		ACC51389	0.847059
c3739	14.4	1.9	17		ABT38540	0.847059
c3740	14.4	1.9	17		ADB05248	0.847059
c3741	14.4	1.9	17		ADB05249	0.847059
c3742	14.4	1.9	17		ADB42730	0.847059
c 324	16.8	2.2	20		ABZ77240	0.84
23979	12.6	1.7	15		AAA47676	0.84
23980	12.6	1.7	15		ABK46570	0.84
c23981	12.6	1.7	15		AAD26136	0.84
c23982	12.6	1.7	15		ABL91829	0.84
10810	13.4	1.8	16		AAT75139	0.8375
10010	13.4	1.0	10		11/11/19	0.0073



	Ger	Core versi	on 5.1.6			
(Copyright ((c) 1993 - 2	004 Compi	ugen Ltd.		
OM nucleic	- nucleic s	earch, using	g sw model			
Run on:	March 29	9, 2004, 16:	:27:20 ; Sea	rch time 74	1.6121 Seconds	
		(witho	ut alignmer	nts)		
		5600.	675 Million	cell update	s/sec	
Title:	US-09-477	-082-2				
Perfect scor	re: 753					
Sequence:	1 aatta	gaccgcgtatt	gaaa	tacactggttt	ttaacctt 753	
_ ·						
Scoring tabl	e: IDENT	TY NUC				
		, Gapext 1	.0			
		, =				
Searched:	682709	seas. 2774	75446 resid	dues		
Total number	er of hits sa	atisfying ch	osen param	eters: 7	18054	
				- · · · · · · · · · · · · · · · · · · ·		
Minimum D	B sea lena	th: 15				
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a.amam L	00q 1011g	,				
Post-proces	sing: Minir	num Match	0%			
		Match 100%				
		65000 sum				
	.ioung mot	55555 3dill	aiios			
Database :	harreel	Patents_N	 A·*		,	-
			na/5A_COM	IR sea·*		
			na/5B_COM			
			na/6A_COM			1
			na/6B_COM			
			na/PCTUS_		<u> </u>	
			na/PC105_ na/backfiles			
	. /cgiiz_6/	piuuala/Z/II	ia/Dackilles	1.3cq.		
Dead M	a ic tha a	imbor of ro	culte prodict	od by obco	co to have a	
					ce to have a	
					being printed,	
and is d	enved by a	analysis of t	the total sco	ne aistribut	IOII.	
		01134345	IEC .			
		SUMMAR	IES .			
		<u>%</u>				
Result		Query	<u> </u>		<u> </u>	
No.	Score	Match	Length	DB	ID	S/L
	4 4	1.9	15		US-08-832-021-28	0.93333
2820	14				LLC 00 075 054 24	0.93333
2820 2821	14				US-08-275-951-31	
		1.9			US-08-087-387-6	0.
2821	14	1.9 1.9	16	1	1	0.
2821 1801	14 14.4	1.9 1.9 1.9	16 16	1	US-08-087-387-6	



c1805	14.4	1.9	16	1	US-08-088-658-34	0.9
1806	14.4	1.9	16		US-08-461-271-6	0.9
1807	14.4	1.9	16	1	US-08-713-685A-6	0.9
1808	14.4	1.9	16	2	US-08-689-856-6	0.9
c1809	14.4	1.9	16	2	US-08-471-907A-34	0.9
1810	14.4	1.9	16	3	US-09-070-477-6	0.9
c1811	14.4	1.9	16	3	US-08-088-661F-9	0.9
c1812	14.4	1.9	16	4	US-08-150-156A-21	0.9
c1813	14.4	1.9	16	. 4	US-08-108-591B-1	0.9
4872	13.4	1.8	15	1	US-08-425-315-1	0.893333
4873	13.4	1.8	15	2	US-08-292-620A-363	0.893333
4874	13.4	1.8	15	2	US-08-292-620A-364	0.893333
4875	13.4	1.8	15	2	US-08-173-489C-45	0.893333
c4876	13.4	1.8	15	2	US-08-173-489C-61	0.893333
4877	13.4	1.8	15	3	US-08-716-190-11	0.893333
4878	13.4	1.8	15	3	US-08-832-021-24	0.893333
4879	13.4	1.8	15	3	US-08-832-021-54	0.893333
4880	13.4	1.8	15	3	US-09-071-845-363	0.893333
4881	13.4	1.8	15	3	US-09-071-845-364	0.893333
2822	14	1.9	16	4	US-09-531-000-9	0.875
7116	13	1.7	15	3	US-08-832-021-25	0.866667
7117	13	1.7	15	3	US-08-832-021-26	0.866667
7118	13	1.7	15	3	US-08-832-021-27	0.866667
1814	14.4	1.9	17	4	US-08-584-040-2548	0.847059
1815	14.4	1.9	17	4	US-08-584-040-2549	0.847059
1816	14.4	1.9	17	4	US-09-371-772B-1072	0.847059
1817	14.4	1.9	17	4	US-09-371-772B-1073	0.847059
4882	13.4	1.8	16	4	US-09-124-238A-4	0.8375
4883	13.4	1.8	16	4	US-09-331-930A-4	0.8375
4884	13.4	1.8	16	4	US-09-721-975-4	0.8375
4885	13.4	1.8	16	4	US-08-894-251A-5	0.8375
4886	13.4	1.8	16	4	US-09-300-958A-56	0.8375
4887	13.4	1.8	16	4	US-09-300-958A-83	0.8375
4888	13.4	1.8	16	4	US-09-986-621-4	0.8375
4889	13.4	1.8	16	4	US-09-527-972-15	0.8375
12749	12.4	1.6	15	1	US-08-087-387-5	0.826667
12750	12.4	1.6	15	1	US-08-455-627-5	0.826667
c12751	12.4	1.6	15	1	US-08-452-196A-6	0.826667
12752	12.4	1.6	15	1	US-07-971-978-1	0.826667
12753	12.4	1.6	15	1	US-08-461-271-5	0.826667
12754	12.4	1.6	15	1	US-08-713-685A-5	0.826667
c12755	12.4	1.6	15	1	US-08-756-728A-2	0.826667
12756	12.4	1.6	15	1	US-08-663-918-3	0.826667
c12757	12.4	1.6	15	1	US-08-663-918-4	0.826667
12758	12.4	1.6	15	2	US-08-689-856-5	0.826667
12759	12.4		15	2	US-08-292-620A-9	0.826667
12760	12.4		15		US-08-292-620A-360	0.826667
12761	12.4		15	2	US-08-292-620A-361	0.826667
12762	12.4		15	2	US-08-292-620A-362	0.826667

	Ger	Core versi	on 5.1.6			
l			004 Comp	igen I td		
<u>-</u> -	Jopyngiit	(0) 1000 2		-9		
-						
OM nucleic	nuclaic s	earch using	n sw model			
OW HUCIER	- Hudielo 3	caron, using	g 3W model			
Run on:	March 29	2004 18	10:30 : Sea	rch time 29	1.04 Seconds	
	1010112		ut alignmer			
			441 Million		s/sec	
I						
Title: \	JS-09-477	-082-2				
Perfect scor						
Sequence:		gaccgcgtatt	gaaa	tacactggttt	ttaacctt 753	
		33-3				
Scoring tabl	e: IDENT	TY NUC				
		, Gapext 1	.0			
	ш р ор	,				
Searched:	245894	6 segs. 186	1504846 re	sidues		
Total number	er of hits s	atisfvina ch	osen param	eters: 1	244038	
Minimum DI	B sea lena	th: 15				
Maximum D						
		,				
Post-proces	sina: Minir	num Match	0%			
		Match 100%				
		65000 sum				
	<u>g</u>					
Database :	Publish	ned Applica	ations_NA:*			
			ubpna/US0		MB.sea:*	
			ubpna/PCT			
3	· /can2 6/	ntodata/1/p	ubpna/US0	6 NEW P	JB.seo:*	
4	· /cgn2_6/	ntodata/1/p	ubpna/US0	6 PUBCO	MB.seg:*	
			ubpna/US0			
			ubpna/PCT			
			ubpna/US0			
			ubpna/US0			
			ubpna/US0			
1	0: /can2 (S/otodata/1/	/pubpna/US	09B PUBC	OMB.seq:*	
					OMB.seq:*	
1:	2: /can2 (3/ptodata/1/	/pubpna/US	09 NEW I	PUB.sea:*	
					OMB.seq:*	
					COMB.seq:*	
1	5: /can2 (3/ptodata/1	/pubpna/US	10C PUBC	COMB.seq:*	
			/pubpna/US			
1	7: /can2 i	6/ptodata/1	/pubpna/US	60 NEW I	PUB.sea:*	
1	8: /can2 i	3/ptodata/1	/pubpna/US	60 PURCO	OMB.sea:*	
	o. rognz_	, productar II	Paspila/00			
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					being printed,	
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and is u	clived by	ariaryoio Ul	inc ioidi 30	oro distribu		

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		SUMMAR	IFS			
		%				
Result		Query			112	
No.	Score	Match	Length	DB	ID	S/L
						O/L
2297	. 14	1.9	15	14	US-10-188-404-31	0.933333
c1457	14.4	1.9	16		US-09-955-410-1	0.9
c1458	14.4	1.9	16		US-09-983-210-21	0.9
c1459	14.4	1.9	16	14	US-10-154-890-1	0.9
c4547	13.4	1.8	15	14	US-10-157-580A-142	0.893333
c 838	15	2	17	14	US-10-338-777-196	0.882353
7072	13	1.7	15	9	US-09-805-296D-12	0.866667
7073	13	1.7	15	14	US-10-072-975-12	0.866667
7074	13	1.7	15	14	US-10-051-436-12	0.866667
7075	13	1.7	15		US-10-360-275-12	0.866667
c 137	16.8	2.2	20	10	US-09-912-724-28	0.84
4548	13.4	1.8	16	9	US-09-811-093-21	0.8375
4549	13.4	1.8	16	9	US-09-777-422-11	0.8375
c4550	13.4	1.8	16	10	US-09-880-313A-42	0.8375
4551	13.4	1.8	16		US-09-997-672-30	0.8375
4552	13.4	1.8	16		US-09-986-625-4	0.8375
c4553	13.4	1.8	16	10	US-09-894-159-64	0.8375
4554	13.4	1.8	16	10	US-09-854-326-11	0.8375
4555	13.4	1.8	16		US-10-362-711-9	0.8375
4556	13.4	1.8	16	14	US-10-136-082-11	0.8375
4557	13.4	1.8	16	14	US-10-163-277-5	0.8375
4558	13.4	1.8	16	14	US-10-136-056-11	0.8375
4559	13.4	1.8	16	14	US-10-261-717-11	0.8375
4560	13.4	1.8	16	14	US-10-284-126-11	0.8375
4561	13.4	1.8	16	14	US-10-283-797-11	0.8375
4562	13.4	1.8	16	14	US-10-283-771-11	0.8375
4563	13.4	1.8	16	14	US-10-261-821-11	0.8375
c4564	13.4	1.8	16	14	US-10-164-915-2	0.8375
4565	13.4	1.8	16	14	US-10-262-258-11	0.8375
4566	13.4	1.8	16	14	US-10-262-264-11	0.8375
4567	13.4	1.8	16	14	US-10-262-252-11	0.8375
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Run on: March	29, 2004, 16	:32:15 ; Sea	arch time 2	894.53 Seconds	s	
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	9153	.537 Million	cell update	es/sec		
Title: US-09-47	7-082-2					
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Searched: 37577	330 seqs, 17	7593059518	residues			
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5275	15.4	2	18	49	US-10-310-188-9840	0.855556
c5276	15.4	2	18	49	US-10-310-188-14825	0.855556

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Run on:	March 28		ut alignmer		3.77 Seconds	
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Searched:	126898	5 seqs, 303	744313 res	idues		
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Result		Query				
No.	Score	Match	Length	DB	ID	S/L
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c1329	13.8	1.8	17		PCT-US03-25614-376	0.820007
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c8191	12.4	1.6	16			
c 46	16.2	2.2	21		US-10-398-483-10 PCT-US04-00035-23548	0.775
c 47	16.2	2.2	21		US-10-786-720-6011	0.771429
135	15.4	2.2	20		US-10-667-275A-7	0.771429 0.77
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205	15.2 15.2	2	21		PCT-US04-00035-31098	0.72381
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	14: gb_est	5:*				
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	16: em_es					
	17: em_gs					
	18: em_gs					
	19: em_gs	s_pln:*				
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	21: em_gs				•	
	22: em_gs	s_mam:*		<u> </u>		

	23: em_gss									
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	25: em_gss									
26: em_gss_phg:*										
	27: em_gss									
	28: gb_gss									
	29: gb_gss									
Pred. No. is the number of results predicted by chance to have a										
score greater than or equal to the score of the result being printed,										
			he total sco							
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		SUMMAR	IES							
		%								
Result		Query								
No.	Score		Length	DB	ID	S/L				
3024	14	1.9	15	10	AW246494	0.933333				
c4962	13		15		CF543203	0.866667				
c3920	13.4		16		CF291803	0.8375				
510	15.8		19		AZ645841	0.831579				
96	17.4		21		AZ647578	0.828571				
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6719	12.4		15		CF290920	0.826667				
6720	12.4				CF291029	0.826667				
6721	12.4		15		CF291029 CF291103	0.826667				
6722	12.4		15		CF291717	0.826667				
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6727	12.4		15		CF295100 CF296652	0.826667				
	12.4		15		CF298032 CF298148					
6728			1			0.826667 0.826667				
6729	12.4	1.6	15		CF298630					
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6732	12.4		15		CF298889	0.826667				
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FEATURES
source
Search completed: March 31, 2004, 14:14:07 Job time: 0.001 secs
                                                                                                                                                                                                                                           Query Match 1.2%; Score 9.2; DB 1; Length 15; Best Local Similarity 78.6%; Pred. No. 0; Matches 11; Conservative 0; Mismatches 3; Indels
                                                                                                                  638 TGCCCAAAAACAA 651
|| ||||||| ||
15 TGATCAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCM7 row: D column: 12

High quality sequence stop: 14.

Licoation/Qualifiers
1. .15
                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xcef="taxon:9606"
/db_xcef="taxon:9606"
/db_xcef="taxon:9606"
/clone="IMAGE:2821595"
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/cell_line="MGC3"
/lab_fnost="POIDB (phage-resistant)"
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/clone_lib="NIH_MGC_7"
/clone_lib="NIH_MGC_7"
/clone_ib="NIH_MGC_7"
/clone_ib="NIH_MGC_7"
/cloned_into_EccRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Result
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AW246494
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9.2
Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information

be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washingtion Genome Center. Vec
                                                                                                                                                                           Unpublished (1999)
Other_ESTs: 2821595.5prime
                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 15)
                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                     AW246494
AW246494.1 GI:6589487
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2821595.3prime NIH_MGC_7
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Copyright (c) 1993 - 2004 Compugen Ltd
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22.590 Million cell updates/sec
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sapiens cDNA clone IMAGE:2821595 3',
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ACCESSION: AW246494
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AW246494/c
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Barkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Mashingtion Genome Center
Trimming: cross match from University of Washingtion Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 14
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 15 contiguous distinct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 15)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Other_ESTs: 2821595.5prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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/clone lib="NIH_MGC_7"
/clone="Grgan: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="GrgAn made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:2821595"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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/db_xref="taxon:9606"
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Pred. No.
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sequence.

Polyadenylation: Based upon the

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; ANTI-SENSE: NO PUBLICATION INFORMATION: DOCUMENT NUMBER: WO PCT/EP92/01220 FILING DATE: 22-MAY-1992 US-09-983-210-21
                                                                                                                                                                                                                                                                                            Sequence 31. Application US/10188404
Publication No. US20030105286A1
GENERAL INFORMATION:
APPLICANT: Egholm, Michael
APPLICANT: Neilsen, Peter
APPLICANT: Buchardt, Ole
APPLICANT: Dueholm, Kim L.
           APPLICANT: Neilsen, Peter
APPLICANT: Buchardt, Ole
APPLICANT: Buchardt, Ole
APPLICANT: Christensen, Leif
APPLICANT: Christensen, Leif
APPLICANT: Coull, James M.
APPLICANT: Cielly, John
APPLICANT: Kielly, John
APPLICANT: Griffith, Michael
TITLE OF INVENTION: Linked Peptide Nucleic Acids
FILE REFERENCE: 18155942
CURRENT APPLICATION NUMBER: US/10/188,404
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 08/275,951
PRIOR FILING DATE: 1994-07-15
PRIOR PPLICATION UMBER: 08/765,798
PRIOR FILING DATE: 1997-04-23
NUMBER: 08/2012-07-15
PRIOR PILING DATE: 1997-04-23
NUMBER: 08/2012-07-15
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APPLICANT: Begholm, Michael
APPLICANT: Nielsen, Peter Eigil
APPLICANT: Nielsen, Peter Eigil
APPLICANT: Berg, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids
FILE REFERENCE: ISISOS40
CURRENT APPLICATION NUMBER: US/10/154,890
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US/08/108,591
PRIOR FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-188-404-31/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10154890 Publication No. US20030180734A1 GENERAL INFORMATION:
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Best Local Similarity 84.6
Matches 11; Conservative
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Best Local
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: No. US20030180734A1el Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 9.8; DB 1; Length 16; Pred. No. 6.7;
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Search completed: March 31, 2004, 14:11:57 Job time : 0.001 secs
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                                                                                                      Query Match
Best Local Similarity 83.3
                                                                                                                                                                                                                                                      SEQ ID NO 31
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
FEATURE:
                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (6)...(7)
OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine,
OTHER INFORMATION: Amino Hexanoic Acid, Lysine Linkage
                                                                                       18 AAAGTAAAAGAA 29
                                                                                                                                   1.2%;
                                                                                                                   Score 8.8; DB Pred. No. 8.1; 0; Mismatches
                                                                                                                                                 1; Length 15
                                                                                                                     2
                                                                                                                      Indels
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APPLICANT: Buchardt, Ole APPLICANT: Egholm, Michael APPLICANT: Nielsen, Peter Eigil APPLICANT: Berg, Rolf Henrik TITLE OF INVENTION: Peptide Nucleic Acids

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                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 08/275,951
PRIOR FILING DATE: 1994-07-15
PRIOR APPLICATION NUMBER: 08/765,798
PRIOR FILING DATE: 1997-04-23
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
SENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                  Query Match
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/154,890
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US/08/108,591
PRIOR FILING DATE: 2001-08-13
PRIOR FILING DATE: 2001-08-13
PRIOR FILING DATE: 2001-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/188,404
CURRENT FILING DATE: 2002-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Griffith, Michael
TITLE OF INVENTION: Linked Peptide Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Egholm, Michael
                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (6)...(7)
OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine,
OTHER INFORMATION: Amino Hexanoic Acid, Lysine Linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: ISIS5042
                                                                                                                                                                                                                                                                                                                   LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                               OTHER INFORMATION: Synthetic construct
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                                        460 CTT
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                                                                                                 Similarity 100.0%;
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Buchardt, Ole
Dueholm, Kim L.
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Coull, James M.
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                                 TCTTT 473
TCTTTT 15
                                                                                               1.9%; Score 14; DB 1; Length 15; 100.0%; Pred. No. 1.5;
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PRIOR APPLICATION NUMBER: DK 0986/91

APPLICATION NUMBER: DK 0987/91

FILING DATE: 24-MAY-1991

PRIOR APPLICATION NUMBER: DK 0987/91

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DK 0510/92

FILING DATE: 15-APR-1992

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LEROTH: 16 Dase pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Nielsen, Peter Eigil
APPLICANT: Nelsen, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleobases
FILE REFERENCE: ISIG4800
CURRENT APPLICATION NUMBER: US/09/955,410
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 08/108,591
PRIOR APPLICATION NUMBER: 09/686,114
PRIOR FILING DATE: 1993-11-22
PRIOR APPLICATION NUMBER: 09/686,114
PRIOR FILING DATE: 1996-07-24
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 11
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APPLICANT: Buchardt, Ole
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/150156
FILING DATE: 1994-APR-05
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0986/91
FILING DATE: 24-MAY-1991
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0: FILING DATE: 2001-OCT-23 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: TH
TITLE OF INVENTION: DI.
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                      TOPOLOGY: li
                                                      TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
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US2002016038331
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                linear
DNA (genomic)
                                       single
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Pred. No. 6
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Sequence 1. Application US/09955410

Patent No. US20020146718A1

GENERAL INFORMATION:

APPLICANT: Buchardt, Ole
APPLICANT: Beys, Rolf Henrik

TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleobases

FILE REFERENCE: ISIG4800

CURRENT APPLICATION NUMBER: US/09/955,410

CURRENT APPLICATION NUMBER: US/09/955,410

CURRENT APPLICATION NUMBER: 08/108,591

PRIOR APPLICATION NUMBER: 09/686,114

PRIOR APPLICATION NUMBER: 09/686,114

PRIOR FILING DATE: 1993-11-22

APRIOR FILING DATE: 1996-07-24

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
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Maximum Match 100%
Listing first 50 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     000
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9.8
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9.8
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seq length: 2000000000
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Match
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US-09-983-210-21

US-10-124-890-1

US-10-188-404-31

US-09-955-410-1

US-09-983-210-21

US-10-148-890-1

US-10-188-404-31
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Compugen Ltd.
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Sequence 21, Appli
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Sequence 21, Appli
Sequence 31, Appli
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; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILLING DATE: 22-MAY-1992
US-09-983-210-21
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; Sequence 21, Application US/09983210
; Patent No. US20020160383A1
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Best Local (
                                                        Matches
                                                                    Query Match
Best Local
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INFORMATION FOR SEQ ID NO: 22
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/
ETILING DATE: 2001-OCT-23
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
ETILING DATE: 1994-APR-05
PRIOR APPLICATION DATA:
APPLICATION UMBER: DK 098
ETILING DATE: 24-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                   TOPOLOGY: 1ir
MOLECULE TYPE:
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-MAY-PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    FILING DATE: 24-MAY-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     715 CTTTTTTTTTTGATC 730
                       715 CTTTTTTTTTTGATC 730
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                                                      1 Similarity
                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                      Conservative
                                                                                                                                                                                        linear
E: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                       24-MAY-1991
                                                                                                                                                                                                                                single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE USE OF NUCLEIC ACID AND DIAGNOSTICS AND ANALYTICAL
                                                                    1.9%; Score 14.4; DI
93.8%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                                                                     DK 0987/91
                                                                                                                                                                                                                                                                                                                          DK 0510/92
                                                                                                                                                                                                                                                                                                                                                                                                               DK 0986/91
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Pred. No. 1
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                                                        Mismatches
                                                                                     DB 1;
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CAL PROCEDURES
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                                                                                  Length 16;
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                                                        Gaps
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RESULT 3 US-10-154-890-1/c

Sequence 1, Application US/10154890 Publication No. US20030180734A1 GENERAL INFORMATION:

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; TOPOLOGY: US-09-070-477-6
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US-08-275-951-31/c
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                                                                                                                        RESULT 30
US-08-832-021-28/c
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CURRENT APPLICATION NUMBER: US/08/275,951

CURRENT APPLICATION NUMBER: US/08/275,951

PRIOR APPLICATION NUMBER: 08/108,591

PRIOR FILING DATE: 1993-07-02

PRIOR PRIOR DATE: 1993-07-02

PRIOR PRIOR DATE: 1993-07-02

PRIOR APPLICATION NUMBER: 08/088,661

PRIOR APPLICATION NUMBER: 9CT/EP92/01219

PRIOR APPLICATION NUMBER: 9CT/EP92/01219

PRIOR APPLICATION NUMBER: 966/91

PRIOR APPLICATION NUMBER: 966/91

PRIOR APPLICATION NUMBER: 986/91

PRIOR APPLICATION NUMBER: 987/91

PRIOR APPLICATION NUMBER: 510/92

PRIOR APPLICATION NUMBER: 510/92

PRIOR FILING DATE: 1991-05-25

PRIOR APPLICATION NUMBER: 510/92

PRIOR PRIOR DATE: 1991-05-26

PRIOR PRIOR PRIOR DATE: 1991-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-275-951-31
Sequence 28, Application US/08832021 Patent No. 6045998 GENERAL INFORMATION: APPLICANT: Combates, N. APPLICANT: Pardinas, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.2%;
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Egholm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31, Application US/08275951 Patent No. 6451968
                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Description of Artificial Sequence: No. 6451968el Sequence NAME/KEY: misc_feature LOCATION: (6)...(7)
OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine, Amino OTHER INFORMATION: Hexanoic Acid, Lysine Linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: Dueholm, Kim L.
PPLICANT: Christensen, Leif
TILE OF INVENTION: Linked Peptide Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT:
                                                                                                                                                                                                                                                                                                                                           Y Match 1.2%;
Local Similarity 83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    643 AAAAAACAAGT 653
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                                                                                                                                                                                                                          14 AAAGAAAAAAA 3
                                                                                                                                                                                                                                                                     18 АЛАСТАЛАДА 29
                                                                                                                                                                                                                                                                                                                      10;
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Coull, James M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neilsen, Peter
Buchardt, Ole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kiely, John
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                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                           Score 8.8; D
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                         Mismatches
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APPLICANT: Parimoo, S.
APPLICANT: Eronuty, S.
APPLICANT: Stenn, K.
TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
FILE REFERENCE: JBP-382
CURRENT APPLICATION NUMBER: US/08/832,021
CURRENT FILING DATE: 1997-04-02
CURRENT FILING DATE: 1997-04-02
CURRENT FILING DATE: 297-04-02
CURRENT FILING DATE: 297-04-02
CURRENT FILING DATE: 1997-04-02
CURRENT FILING DATE: 1997-04-02
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
COTHER THOODERSTON: Description of Artificial Sequence. Dates
FEATURE:
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                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: primer US-08-832-021-28
                                                                                        Matches
                                                                                                                                 Query Match
                                                           Local Similarity 90.0%; hes 9; Conservative
                                           642 CAAAAAACAA 651
13 CAAAAAAAAA
                                                                                      0; Mismatches
                                                                                                           Score 8.4;
Pred. No. 3
                                                                                                                                   DB 1;
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                                                                                                                                 Length 15
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Search completed: March 31, 2004, 14:10:54
Job time: 0.001 secs

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Matches
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FILING DATE:
APPLICATION NUMBER: 08/087,38*
FILING DATE: 2-Jul-93
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 358-785
TELEPAX: (415) 358-785
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       Sequence 6, Application US/08689856
Patent No. 5830658
GENERAL INFORMATION:
APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
TITLE OF INVENTION: Connected Macromolecular Structures
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
Annuares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
             ZIP: 94306-2155

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Oligonucleotide clamps having diagnostic TITLE OF INVENTION: and therapeutic applications NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS: ADDRESS: Stephen C. Macevicz, Lynx Therapeutics STREET: 465 Lincoln Centre Drive CITY: Foster City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Microsoft Word for Windows, vers. 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,685A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch diskette
                                                                                                                                                                                     STREET: Five Palo
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM compatible OPERATING SYSTEM: Windows 3.1/DOS 5.0
  APPLICATION NUMBER:
                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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Five Palo Alto Square, 3000 El Camino Real
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                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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90.9%; Pred. No. 26;
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US/08/689,856
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RESULT 28
US-09-070-477-6/c
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                               NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 358-7855
TELEPAX: (415) 358-7994
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 90.9%;
Matches 10; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application Patent No. 6048974
GENERAL INFORMATION:
APPLICANT: Sergei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-857-0663
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/08/455,627
APPLICATION NUMBER: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
STREET: 465 Lincoln Centre Drive
CITY: Foster City
STRIE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                           FILING DATE: 08/01
APPLICATION NUMBER: 08/01
FILING DATE: 2-Jul-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: 5.25 inch diskette
COMPUTER: IBM compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
TITLE OF INVENTION: and therapeutic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Nakamura, Jackie N.
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: LY.
BLECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: size TOPOLOGY: linear
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/461,271
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              nucleic acid
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Pred. No. 26;
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RESULT 24
US-08-455-627-6/c
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COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers. 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,387
FILING DATE: 19930702
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ETILING DATE: TOTATE: 
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Best Local Similarity 90.9%;
                                                                       COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION UNMER: US/08/455,627
FILLING DATE: 31-MAY-1995
CULASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NAKAMULTA, Jackie N.
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: 35,966
REFERENCE/DOCKET NUMBER: 15.000
TELEPHONE: 415-843-5000
TELEPHONE: 415-843-5000
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APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
TITLE OF INVENTION: Connected Macromolecular Structures
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
TELEFAX: 415-857-0663
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 358-7794
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Stephen C. Macevicz REGISTRATION NUMBER: 30,285 REFERENCE/DOCKET NUMBER: 104 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 358-7855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: 5.25 in
COMPUTER: IBM compat
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
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Pred. No. :
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RESULT 26 US-08-713-685A-6/c

Sequence 6, Application US/08713685A Patent No. 5817795 GENERAL INFORMATION:

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Patent No. 5741643
GENERAL INFORMATION:
                                                          Matches
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Best Local
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INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,
FILING DATE: 2-011-93
ATTORNEY,AGENT INFORMATION:
NAME: Stephen C. Macevicz
                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 358-7855
TELEPAX: (415) 358-7794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITLE OF INVENTION: Oligonuclectide clamps having diagnostic of INVENTION: and therapeutic applications
                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM compatible OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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10; Conserv
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F: 465 Lincoln Centre Drive
Foster City
California
                                                                       Similarity
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Pred. No. 26;
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US-08-150-156A-21
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CURRENT APPLICATION NUMBER: US/08/088,661F
CURRENT FILING DATE: 1993-07-02
PRIOR APPLICATION NUMBER: 08/054,363
PRIOR PILING DATE: 1993-04-26
PRIOR PPLICATION NUMBER: PCT/EP92/01219
PRIOR FILING DATE: 1992-05-19
PRIOR FILING DATE: 1992-05-19
PRIOR PILING DATE: 1992-05-19
PRIOR FILING DATE: 1992-05-19
PRIOR PILING DATE: 1992-05-19
PRIOR PILING DATE: 1992-05-19
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SEQ ID NO 9
                                                                                                                                                                                                                                                       Sequence 21, Application US/08150156A Patent No. 6357163 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
              SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/150,
FILLING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0986/91
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                      TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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APPLICATION NUMBER: FILING DATE: 24-MAY
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al Similarity 84.6%;
11; Conservative
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Wittung, Pernilla
Buchardt, Ole
Egholm, Michael
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 24-MAY-1991
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                                                                    US/08/150,156A
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Pred. No. 25;
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US-08-108-591B-1
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                                                                                                                                                          RESULT 23
US-08-087-387-6/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Buchardt, Ole
APPLICANT: Bytholm, Michael
APPLICANT: Nielsen, Peter Eigil
APPLICANT: Berg, Rolf Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 051
PILING DATE: 15-APR-1992
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                            Sequence 6, Application US/08087387
Patent No. 5473060
GENERAL INFORMATION:
APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Oligonucleol
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Berg Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids
FILE REFERENCE: ISISS540
CURRENT APPLICATION NUMBER: US/08/108,591B
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vequence 1, Application US/08108591B
Patent No. 6395474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0987/91
FILING DATE: 24-MAY-1991
             CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
STREET: 465 Lincoln Centre Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOCUMENT NUMBER: WO PCT/EP92/01220 FILING DATE: 22-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
CITY: Foster City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH:
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                                                                                                                                                                                                                                                            640
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                                                                                                                                                                                                                                                            CCCAAAAAACAAG 652
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                                                                   Oligonucleotide clamps having diagnostic andtherapeutic applic
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Pred. No. 25;
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RESULT 18
US-08-088-658-34
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COUNTY:
2IP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: Release #1.0, Version #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.3%;
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5641625
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 215-568-310
TELEFAX: 215-568-3439
INFORMATION FOR SQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NO TITLE OF INVENTION: OL NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF TITLE OF INVENTION: NUCLEIC ACIDS NUMBER OF SEQUENCES: 56
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                 STATE: F
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                                                                                                                                                                                  STREET: One Liberty CITY: Philadelphia
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EDNESS: single
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                                                                                                                                                                                                                                                                                                                       Nielsen, Peter E.
Berg, Rolf H.
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Egholm, Michael
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Pred. No. 25
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US-08-471-907A-34
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GENERAL INFORMATION:
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Best Local S
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TELEFAX: 215-568-3439 INFORMATION FOR SEQ ID NO:
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REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: IS
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 08/054,363
FILING DATE: 26-APRIL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5986053ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,907A
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                               NAME: Lucci, Joseph
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: IS:
TELECOMMUNICATION INFORMATION:
                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                             ATTORNEY/AGENT INFORMATION:
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APPLICANT: M llegaard, Niels E.
IITLE OF INVENTION: HIGH ORDER STI
                                                                                                                                                                                                                                                                                                                                                                   STREET: Out ______CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: sing
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                                 TELEPHONE:
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Egholm, Michael
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                                                                ISIS-1052
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                                                                            SOFTWARE: PA
SEQ ID NO 31
LENGTH: 15
TYPE: DNA
                                                                                                                                                                   PRIOR FILING DATE: 1992-05-22
PRIOR APPLICATION NUMBER: 986/9
PRIOR FILING DATE: 1991-05-22
PRIOR APPLICATION NUMBER: 987/9:
PRIOR FILING DATE: 1991-05-24
PRIOR APPLICATION NUMBER: 510/92
PRIOR FILING DATE: 1991-04-15
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/08/275,951
CURRENT FILING DATE: 1994-07-15
PRIOR APPLICATION NUMBER: 08/1108,591
PRIOR FILING DATE: 1993-11-22
PRIOR FILING DATE: 1993-11-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: JBP-382
CURRENT APPLICATION NUMBER: US/08/832,021
CURRENT FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Parimoo, S.
APPLICANT: Prouty, S.
APPLICANT: Stenn, K.
APPLICANT: Stenn, K.
TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Buchardt, Ole
APPLICANT: Dueholm, Kim L.
APPLICANT: Christensen, Leif
TITLE OF INVENTION: Linked Peptide Mucleic Acids
FILE REFERENCE: ISIS1577
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                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IO ID NO 28
IENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                  THER INFORMATION: Description of Artificial Sequence: No. 6451968el Sequence
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/
FILING DATE: 1993-07-02
APPLICATION NUMBER: 08/
FILING DATE: 1993-07-02
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No. 6045998
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                                                                                                                                        PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kiely, John
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100.0%; Pred. No.
                                                                                                                                                                                             510/92
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RESULT 17
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                                                                                                        Query Match 1.3%;
Best Local Similarity 84.6%;
Matches 11; Conservative
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Patent No. 56291
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Best Local Similarity
                                                                                                                                                                                                                                                                TELEFAX: 215-568-3439 INFORMATION FOR SEQ ID NO:
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APPLICANT: Raviku
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US FILING DATE: N/A CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 16
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION : INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5669152ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
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                                                                          640 CCCAAAAAACAAG 652
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                                            4 CCAAAAAAAAAAG 16
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100.0%; Pred. No.
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                                                                                                                        Score 9.8; I
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US-08-283-591-25

Sequence 25, Application US/08283591 Patent No. 5629152 GENERAL INFORMATION:

APPLICANT:

Ravikumar, Vasulinga

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RESULT 12
US-08-150-156A-21/c
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CURRENT APPLICATION NUMBER: US/08/08/661F
CURRENT FILING DATE: 1993-07-02
PRIOR APPLICATION NUMBER: 08/054,363
PRIOR FILING DATE: 1993-04-26
PRIOR APPLICATION NUMBER: PCT/EP92/01219
PRIOR FILING DATE: 1992-05-19
PRIOR FILING DATE: 1992-05-19
NUMBER OF SEQ ID NOS: 42
SOPTWARE: Patentin Ver: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
Sequence 21, Application US/08150156A Patent No. 6357163
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: THE USE OF NU
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 358-78
TELEFAX: (415) 358-7794
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nielsen, P
APPLICANT: Berg, Rolf
TITLE OF INVENTION: D
                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 16
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APPLICATION NUMBER: 08/0
FILING DATE: 2-Jul-93
ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
TOPOLOGY: linear
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Local Similarity 93.8%;
les 15; Conservative (
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Wittung, Pernilla
Buchardt, Ole
Egholm, Michael
                                                                                                                                                                                  CTTTTTTTTTGGATC 1
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                                                                                                                                                                                                                                                                        1.9%; Score 14.4;
93.8%; Pred. No. 4.
     THE USE OF NUCLEIC ACID ANALOGUES IN DIAGNOSTICS AND ANALYTICAL PROCEDURES
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Pred. No. 4
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CURRENT APPLICATION NUMBER: US/08/108,591B
CURRENT FILLING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
COMMENT OF SERVICES SERVICES SERVICES
FOR THE ORGANISM: ARTIFICIAL NO CONTACT SERVICES
FOR THE ORGANISM: ARTIFICAL NO CONTACT SERVICES
FOR THE ORGANISM SERVICES
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FILING DATE: 15-APR-1992
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
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                                                                                                                                        Matches
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Patent No. 6395474
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Best Local (
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Best Local Similarity 93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Buchardt, Ole
APPLICANT: Egholm, Michael
APPLICANT: Nielsen, Peter Eigil
APPLICANT: Berg, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids
FILE REFERENCE: ISISO540
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MOLECULE TYPE:
HYPOTHETICAL: N
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PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO PCT/EP92/01220
FILING DATE: 22-MAY-1992
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APPLICATION NUMBER: DK 0:
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 24-MAY-
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15; Conserv
                                                                CTTTTTTTTTTGATC 730
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                                                                                                                                     Score 14.4; D
Pred. No. 4.3;
O; Mismatches
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Pred. No. 4.3;
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                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                     Length 16;
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
TENGITH: 16 nucleotides
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Patent No. 5830658
                                                                                                                                                                                   Sequence 34, Application US/08471907A
Patent No. 5986053
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Best Local S
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,856
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/455,627
FILING DATE:
13-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Jakie N.
NAME: Nakamura, Jakie N.
                                                                                                                                                                       GENERAL
                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Nakamura, Jackie N.
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKST NUMBER: LYNX-003/01 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
TITLE OF INVENTION: Connected Macromolecular Structures
                                            TITLE OF INVENTION:
                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Five Far
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                           459 ACTITITITITITIT 474
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CANT: Sergei M.
                                                                                                                                                                      INFORMATION:
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Five Palo Alto Square, 3000 El Camino Real
Nielsen, Peter L.
Nielsen, Peter L.
Berg, Rolf H.
M llegaard, Niels E.
N'ENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
                                                                                                                       Buchardt, Ole
Egholm, Michael
                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09070477 Patent No. 6048974
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lucci, Joseph REGISTRATION NUMBER: 33,307 REFERENCE/DOCKET NUMBER: IS: TELECOMMUNICATION INFORMATION: 215.568-3100
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
TITLE OF INVENTION: and therapeutic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                        STREET: 465 Lincoln Centre Drive CITY: Foster City STATE: California
                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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                                                                                                                                                                                                                                        COUNTRY: USA
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APPLICATION NUMBER: 08/461,271
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                                 JICATION NUMBER:
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93.8%; Pred. No. 4
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                               US/08/713,685
                                                                                                     US/09/070,477
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US-08-461-271-6
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Patent No. 5741643
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                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Oligonuclectide clamps having diagnostic
TITLE OF INVENTION: and therapeutic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy datisk
COMPUTER: IBM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/088,658
FILING DATE: 1930702
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TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
TITLE OF INVENTION: NUCLEIC ACIDS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,363
FILING DATE: 26-APRIL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lucci, Joseph
                                                             COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,271
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch diskette
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REFERENCE/DOCKET NUMBER: ISIS-1052
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                              STREET: 465 Lincoln Centre Drive
CITY: Foster City
STATE: California
FILING DATE:
CLASSIFICATION: 435
RIOR APPLICATION DATA:
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TOPOLOGY: linear
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CITY: Philadelphia
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93.8%; Pred. No. 4.3;
vative 0; Mismatches
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US-08-713-685A-6
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TELEPHONE: (415) 358-7794
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
                                                     US-08-713-685A-6
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Best Local :
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Query Match
Best Local Similarity
                                                                                                                                                             REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 358-7855
TELEPAX: (415) 358-7794
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/087,38
FILING DATE: 2-041-93
ATTORNSY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKST NUMBER: 104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 358-7855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06
FILING DATE:
APPLICATION NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
STREET: 465 Lincoln Centre Drive
CITY: Foster City
STATE: California
                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
                                                                                                                                                                                                                                                                      FILING DATE: 2-Jul-93
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sergei M. Gryvarnov
TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
TITLE OF INVENTION: and therapeutic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                        STRANDEDNESS: single
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                                                                                                         nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM: Windows 3.1/DOS 5.0 Microsoft Word for Windows,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM compatibl
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 1.9%;
93.8%;
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Pred. No. 4.
   Score 14.4; DB 1;
Pred. No. 4.3;
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TOPOLOGY: US-08-283-591-16
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GENERAL INFORMATION:
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NAME: NAKAMULA, JACKLE N.
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: LYNX-003/01 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEPHONE: 415-843-5000
TELEPHONE: 415-857-0663
INFORMATION FOR SEQ ID NO: 6:
                                                                                                      TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                           REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: One Liberty CITY: Philadelphia STATE: PA
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and ADDRESSEE: No. 5629152ris
STREET: One Liberty Place - 46th Floor
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                                  STRANDEDNESS:
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                                                                       ENGTH:
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                   linear
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                                single
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                                 US-08-088-658-34/c
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                                                     RESULT 5
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Sequence 34, Application US/08088658 Patent No. 5641625
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US
FILING DATE: N/A
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ravikumar, Vasulinga
TITLE OF INVENTION: NOVEL TRISUBSTITUTED
TITLE OF INVENTION: OLIGO -LACTAMAMIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPAX: 215-568-3439
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ATTORNEY/AGENT INFORMATION:
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CITY: Philadelphia
STATE: PA
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STRANDEDNESS: sing
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ADDRESSEE: No. 5629152ris
STREET: One Liberty Place - 46th Floor
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93.8%; Pred. No. 4.3;
ative 0; Mismatches
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GENERAL INFORMATION:

APPLICANT:

Ecker, Da Buchardt,

David J.

Egholm, Michael Nielsen, Peter E. Berg, Rolf H.

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2004, 14:10:54; Search time 0.001 Seconds (without alignments)
358.428 Million cell updates/sec
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Title: us094770822

Perfect score: 753

Sequence: 1 aattagaccgcgtattgaaa.....tacactggttttttaacctt 753

Scoring table: IDENTITY NUC Gapext 0.5

Searched: 15 seqs, 238 residues

Total number of hits satisfying chosen parameters:

30

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

Database : 2rni.db:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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quence 6, quence 6, quence 6, quence 6, quence 6, quence 31 quence 28		equence 6, Appilequence 6, Appilequence 6, Appilequence 34, Appilequence 9, Appilequence 21, Appelequence 21, Appilequence 21	scriptio	

ALIGNMENTS

US-08-455-627-6 US-08-455-627-6 IS-equence 6, Application US/08455627 ; Sequence 6, Application US/08455627 ; Patent NO. 5571677 ; Patent NO. 5571677 ; GENERAL INFORMATION: Sergei M. Gryaznov APPLICANT: Sergei M. Gryaznov ITILE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Convergent Synthesis of Branched and Multiply ITITLE OF INVENTION: Sergent Synthesis of Branched and Multiply ITITLE OF INVENTION	Query Match Query Match Best Local Similarity 93.8%; Pred. No. 4.3; Best Local Similarity 93.8%; Pred. No. 4.3; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 15; Conservative 1474 Qy 459 ACTITITITITITITITITITITITITITITITITITITI	8087387 8087387 Robotide clamps having diagnostic andtherapeutic macevicz, Lynx Therapeutics intre Drive a diskette le le le le le diskette le
•		applic

31-OCT-2000 (first entry)

Antisense primer for untreated CASP8 wild type DNA.

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RESULT 10
ADE43355/c
ID ADE433
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                                                                                                                                                                                                                                                                                                       Investigation of silencing of caspase-8 (CASP8) gene by methylation was CC analyzed using methylation-sensitive PCR analysis. Amplification of the CS 'untranslated region (UTR) of the Casp8 gene was performed in reaction CC mixtures containing bisulfite treated DNA. Primers AAAS1818-23 were CC gene extending from nucleotides +221 to +541. Wild type primers were used to amplify the corresponding region of untreated genomic DNA. Controls CC without DNA were also performed. CASP8, a cysteine protease, is part of Ct the death inducing signaling complex (DISC) associated with the Fas CC receptor. CASP8 is inactivated in cancers, and plays a role of a tumour Suppressor gene. The CASP8 promoter region sequences, in particular CC Region 1 and Region 2, are crucial to the design and execution of the CC genomic methylation PCR analysis of CASP8 gene inactivation. Methylation PCR can be used to examine even minute amounts of patient material to CC demonsrate whether the CASP8 gene expresses an mRNA and protein product. The CASP8 gene has been localized to human chromosome 293-34. The CC EASP8 gene has been localized to human chromosome 293-34. The CC EASP8 gene has been localized to human chromosome 293-34. The CC entraction a vector that expresses a gene expresses a tumour in which a myc cells. The cancer that is diagnosed or treated is a tumour in which a myc cells. The cancer that is diagnosed or treated is a tumour in which a myc cells. The cancer that is diagnosed or treated is a tumour in which a myc cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma, colorectal carcinoma, or uterine cervical carcinoma can be diagnosed with the new method. A kit for screening for a compound that induces death-receptor-mediated apoptosis in cells containing an incomposition of the containing an incomposition of the containing and the provided
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Matches 11
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                                           ADE43355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 61; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or prognosing cancer, comprises detecting a modification of genomic DNA comprising the CASP8 gene that results in inactivation of the gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-452423/39
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                                              DNA;
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78.6%;
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ADE43355

Search completed: March 31, 2004, 14:10:08 Job time : 0.001 secs

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Best Loc Matches Query Match

Local

Similarity

11;

Conservative

0

Mismatches

Indels

0

Gaps

0

Pred Score 8.6;

.1; 1; 4.

Length 20

208 19

ACAGGGCTGTGGGGG

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25-OCT-2001; 2001US-0339525P.
08-NOV-2001; 2001US-0336929P.
08-NOV-2001; 2001US-0338010P.
09-NOV-2001; 2001US-0338363P.
04-DEC-2001; 2001US-0337052P.
28-MAR-2002; 2002US-0368919P.
                                                                        predisposition for or the occurrence of neurodegenerative disease in a subject. The method comprises detecting in a target nucleic acid obtains from the subject the presence or absence of an allelic variant of one or more polymorphic regions of one or more genes selected from upa (Urokinase plasminogen activator). SNCG (gamma-synuclein), IDE (insulindegrading enzyme), KNSLI (Kinesin-like protein 1), LIPA (1960somal acid lypase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the polymorphic regions is indicative of a predisposition for or the occurrence of neurodegenerative disease. The genes are all located on chromosome 10. M1 is useful for determining a predisposition for or the occurrence of, and for treating neurodegenerative disease, particularly Alzheimer's disease. The present sequence is a PCR primer, which was use in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human uPA primer, SEQ ID 524
                                                                                                                                                                                                                                                                                         The
                                                                                                                                                                                                                                                                                                                                                                 Determining a predisposition for or the occurrence of neurodegenerative disease, e.g. Alzheimer's disease by detecting in a target nucleic acid the presence or absence of an allelic variant of one or more polymorphic
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                                                Sequence 20
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                                                                                                                                                                                                                                                                                                                      4; Page 313; 848pp;
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, Mullin KM,
                                                BP;
                                                                                                                                                                                                                                                                                         invention relates to a method (M1) for determining
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1.1%;
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Sampson AJ,
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                                                T; 0 U; 0 Other;
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                                                                                                                                                                                                                                              cleic acid obtained variant of one or
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AAQ20008 standard; DNA; 16 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methods are used to diagnose or prognose cancer. Cancer is treated by administering a vector that expresses a gene encoding functional CASP8 in cells. The cancer that is diagnosed or treated is a tumour in which a myc gene is amplified, such as a neuroblastoma. Aggressive neuroblastoma, juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma can be diagnosed with the new method. A kit for screening for a compound that induces death-receptor-mediated apoptosis in cells containing an inactivated Chang care in the cartinate of the cartinate 
The 3' end of this oligonucleotide carries 1,3-propanediol. The o one of four oligonucleotides which were designed to specifically cross-link to the duplex target sequence AAQ20004. Oligo #4 with internal cross-linking group was less effective than the other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     deoxyribonucleic acid; major groove; ethanoamino group; aziridinylcytosine; cross-linking group; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
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                                                                                                                                                                                                                  New sequence-specific non-photo-activated crosslinking
                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-1990;
14-JAN-1991;
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                                                                                                                                     Example
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                                                                                                                                                                                                                                                                                                                                                  Matteucci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-1990;
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                                                                                                                                                                                      infections e.g.
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                                                                                                                                   2; Page 21; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         GILEAD
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91US-00640654.
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                                                                                                                                                                                                                                                                                                                                                                                                         SCIE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #4 able to covalently cross-link to target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "N4N4-ethanocytosine"
                                                                                                                                                                                                               of duplex DNA and are esp. useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
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Pred. No. 5.1;
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                            The oligo cally bind with its
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RESULT 8
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ID AX18362/
ID AX1
AX AA11
AX AA11
AX AA11
AX AA11
AX AT-P
XX RT-P
XX PF 18-J
XX O9-F
XX UP1,
PM O9-F
XX UP1,
PM PPT PCR.
XX PT PCR.
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CC This
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                                                                                                                                          This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta 'N3'; or (X)m5'-(gamma)k-delta-N3'; where X = alabelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine or thymine; N = natural number of 3 or over indicating the repetition of gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine; guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene
                                                                                                                                                                                                                                                                                                                                       Peptides PCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oligonucleotides with terminal cross-linking groups.
                                                                                                       Sequence 16
                                                                                                                               sequences
                                                                                                                                                                                                                                                                                                             Disclosure; Page 10; 19pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-1997;
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Similarity 91.7%;
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Pred. No. 8.4;
                                                   Mismatches
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RESULT 9
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AAA51823 standard; DNA; 21

ВP

AAA51823;

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RRESULT 5
ANATIBAGE
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ID ANATIBAGE
XX ANATIBAGE
XX RT-P
XX RT-P
XX RT-P
XX PPI
PF 18-J
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX18362;
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                      Disclosure; Page 10; 19pp; Japanese
                                                                                                                                                                                                                                                              18-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      RT-PCR primer; DNA sequence determination;
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91US-00640654.
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/mod_ba
                                                                                         least
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
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                                                                                         two
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID
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                                                                                         nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      gene sequence analysis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                         useful
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888888888888888
                                                                                     to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = a denine, guanine or cytosine; N = adenine, guanine or cytosine; N = adenine, guanine or cytosine; N = adenine, guanine cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene
                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X) mS' - (alpha) n-beta
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Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Matches Query Match Best Local 15; Similarity Conservative 1.9%; 0 Score Pred. Mismatches 14.4; No. 3 BB ۳. Length Indels 0 Gaps 0

밁 S 461 TTTTTTTTTTTTTCA 476 TTTTTTTTTTTTCA 16

.822/c σ

AAA51822 standard; DNA; 21 망

AAA51822;

31-OCT-2000 (first entry)

Sense primer for untreated CASP8 wild type DNA.

tumour suppressor; death receptor; apo CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease; or; chromosome 2q33-34; neuroblastoma; cancer apoptosis; cytostatic; gene therapy; primer; cancer; S S S

Homo sapiens

WO200039347-A1

06-JUL-2000

30-DEC-1999; 99WO-US031280

31-DEC-1998; 98US-0114308P

(SJUD-) ST JUDE CHILDREN'S RES

Kidd ٧J, Lahti JM, Teitz T;

WPI; 2000-452423/39

Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or prognosing cancer, comprises detecting a modification of genomic DNA comprising the CASP8 gene that results in inactivation of the gene.

Example 3; Page 61; 107pp; English.

Investigation of silencing of caspase-8 (CASP8) gene by methylation was analyzed using methylation-sensitive PCR analysis. Amplification of the 5 untranslated region (UTR) of the Casp8 gene was performed in reaction mixtures containing bisulfite treated DNA. Primers AAA51818-23 were designed to produce a 320 bp fragment in the upstream region of Casp8 gene extending from nucleotides +221 to +541. Wild type primers were used to amplify the corresponding region of untreated genomic DNA. Controls without DNA were also performed. CASP8, a cysteine processe, is part of the death inducing signaling complex (DISC) associated with the Fas receptor. CASP8 is inactivated in cancers, and plays a role of a tumour suppressor gene. The CASP8 promoter region sequences, in particular Region 1 and Region 2, are crucial to the design and execution of the genomic methylation PCR analysis of CASP8 gene inactivation. Methylation used

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Investigation of silencing of caspase-8 (CASP8) gene by methylation was analyzed using methylation-sensitive PCR analysis. Amplification of the Caspa gene was performed in reaction of intractive containing bisulfite treated DNA. Primers AAA51818-23 were designed to produce a 320 bp fragment in the upstream region of Caspa gene extending from nucleotides +221 to +541. Wild type primers were used to amplify the corresponding region of untreated genomic DNA. Controls complify the corresponding region of untreated genomic DNA. Controls complex (DISC) associated with the Fas creceptor. CASPB is inactivated in cancers, and plays a role of a tumour suppressor gene. The CASPB promoter region sequences, in particular complex (DISC) associated with the Fas creceptor methylation PCR analysis of CASPB gene inactivation. Methylation PCR can be used to examine even minute amounts of patient material to the CASPB gene head to diamons or promose an mRNA and protein product. The CASPB gene hoseled to human chromosome 2q33-34. The
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methods are used to diagnose or prognose cancer. Cancer is treated by administering a vector that expresses a gene encoding functional CASP8 in cells. The cancer that is diagnosed or treated is a tumour in which a myo gene is amplified, such as a neuroblastoma. Aggressive neuroblastoma, juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or prognosing cancer, comprises detecting a modification of genomic DNA comprising the CASP8 gene that results in inactivation of the gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kidd VJ, Lahti JM,
                     WO2003054143-A2
                                                                                         Neurodegenerative disease; uPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6; Alzheimer's disease; neuroprotective; nootropic; gene therapy; Chromosome 10; PCR; primer; ss.
                                                                                                                                                                   Human uPA
                                                                                                                                                                                                         29-JAN-2004
                                                                                                                                                                                                                                                                               ADE43355 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma be diagnosed with the new method. A kit for screening for a compound induces death-receptor-mediated apoptosis in cells containing an tivated CASP8 gene is also provided
                                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                                                            388
                                                                                                                                                                                                                                                                                                                                                                       21 CGCCTCGAATGCAGATACACG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                   primer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 3 A;
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                                                                                                                                                                   SEQ ID 524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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RESULT 4
AAQ2000
ID AAQ2
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XX AAQ2
XX O1-A
XX O1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method (MI) for determining a CC subject. The method comprises detecting in a target nucleic acid obtained from the subject the presence or absence of an allelic variant of one or more polymorphic regions of one or more genes selected from upa CC (Urokinase plasminogen activator), SNCG (gamma-symuclein), IDE (insulin-CC degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid CC lypase), and THEREFS (Tumour Neorosis Factor Receptor-SF6), where the presence of at least one of the allelic variant of one or more CC presence of at least one of the allelic variant of one or more CC cocurrence of neurodegenerative disease. The genes are all located on CC chromosome 10, MI is useful for determining a predisposition for or the CC cocurrence of, and for treating neurodegenerative disease, particularly C Alzheimer's disease. The present sequence is a PCR primer, which was used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-2001;
04-DEC-2001;
28-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining a predisposition for or the occurrence of neurodegenerative disease, e.g. Alzheimer's disease by detecting in a target nucleic acid the presence or absence of an allelic variant of one or more polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page 313; 848pp; English
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                                                                                                                                                                                                                                                                                                                                                 01-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ20008 standard; DNA; 16
                                                                                                                                                                                                                                                                                         Oligonucleotide #4 able to covalently cross-link to target
                                                                                                                                                                                                                                                                                                                                                                                                   AAQ20008;
                                                                                                                                                                                                             aziridinylcytosine; cross-linking group;
                                                                                                                                                                                                                                      deoxyribonucleic acid; major groove; ethanoamino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in the method of the invention.
                                                                           modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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2001US-0337052P.
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                                                                                 Location/Qualifiers
                         /*tag= a
/mod_base=
     note= "N4N4-ethanocytosine"
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100.0%; Pred. No.
                            base= OTHER
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G;
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Blacker DL;
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Scoring table:
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IDENTITY_NUC Gapop 10.0 , Gapext 0.
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Copyright (c) 1993 - 2004 Compugen
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Million cell
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Total number 얁 hits satisfying chosen parameters:

10

seqs, 94 residues

Minimum Maximum DB DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

Database 2rng.db:*

pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pu and is derived by analysis of the total score distribution. printed,

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20	21	16	16	21	16	16	20	21	21	Length DB
ب	щ	۳.	Н	Ь	Н	Н	μ	μ	_	E B
ADE43355	AAA51823	AAX18362	AAQ20008	AAA51822	AAX18362	AAQ20008	ADE43355	AAA51823	AAA51822	ID
Human uPA primer,	Antisense primer i	KI-PCK primer of c	Oligonucleotide #4	Sense primer for u	RT-PCR primer of t	Oligonucleotide #4	Human uPA primer,	Antisense primer i		Description

ALIGNMENTS

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1 TAGGGGACTCGGAGACTGCGA

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CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease; tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer; death receptor; apoptosis; cytostatic; gene therapy; primer; ss.
                                                                                     Sense primer
                                                                                                        31-OCT-2000
                                                                                                                                             AAA51822 standard; DNA;
                                                                                      for untreated CASP8
                                                                                                        (first
                                                                                                        entry)
                                                                                                                                               21
                                                                                                                                               BP
                                                                                       wild
                                                                                      type
                                                                                       DNA
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Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or prognosing cancer, comprises detecting a modification of genomic DNA comprising the CASP8 gene that results in inactivation of the gene. 30-DEC-1999; 06-JUL-2000 WPI; 2000-452423/39. Example 3; Page 61; 107pp; English. (SJUD-) ST JUDE CHILDREN'S RES Ų, Lahti JM, 99WO-US031280 HOSPITAL

Investigation of silencing of caspase-8 (CASP8) gene by methylation was call analyzed using methylation-sensitive PCR analysis. Amplification of the Casp8 comixtures containing bisulfitte treated DNA. Primers AAA51818-23 were mixtures containing bisulfitte treated DNA. Primers AAA51818-23 were call designed to produce a 320 bp fragment in the upstream region of Casp8 companies the corresponding region of untreated granding DNA. Controls to amplify the corresponding region of untreated granding DNA. Controls complex (DNA) associated with the Fas corresponding signaling complex (DISC) associated with the Fas corresponding signaling complex (DISC) associated with the Fas corresponding signaling complex (DISC) associated with the Fas corresponding to the death inducing signaling complex (DISC) associated with the Fas corresponding signaling complex (DISC) associated with the Fas corresponding to the design and execution of the genomic methylation pCR analysis of CASP8 gene inactivation. Methylation pCR canalysis of CASP8 gene inactivation. Methylation pCR canalysis of CASP8 gene inactivation. Methylation pCR canalysis of CASP8 gene inactivation and product corresponding even minute amounts of patient material to pCR can be used to examine even minute amounts of patient material to the CASP8 gene has been localized to human chromosome 2q33-34. The corresponding even as a pencencer. Cancer is treated by administering a vector that expresses a gene encoding functional CASP8 in call the suppose of the cappes in the carcinomal corresponding correspondin cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma can be diagnosed with the new method. A kit for screening for a compound that induces death-receptor-mediated apoptosis in cells containing an inactivated CASP8 gene is also provided

Sequence 21 BP; 5 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Ś Matches Query Match Best Local 90 Similarity TAGGGGACTCGGAGACTGCGA 110 Conservative 100.0%; 2.8%; 0; Mismatches Score 21; Pred. No. DB 1; Length 21; 0.52; Indels 0, Gaps 0

RESULT 2
AAAS1823/c
ID AAAS18
XX AAAS18
AC AAAS18
XX 31-OCT
XX Antise
XX Antise
XX CASP8;
KW tumour
KW tumour
KW tumour
XX Homo s
XX Y
PN WO2000 AAA51823; AAA51823 standard; DNA; 21 BP

31-OCT-2000

(first entry)

Antisense primer for untreated CASP8 wild type DNA.

CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease; tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer; death receptor; apoptosis; cytostatic; gene therapy; primer; ss.

WO200039347-A1

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REFERENCE
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I28367/c
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I16032/c
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Best Local Similarity 90.9%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unknow...
Unclassified.
1 (bases 1 to 16)
1 (bases 1, to 16)
Gryaznov, S.M.
Convergent synthesis of branched and multiply connected macromolecular structures
Patent: US 5830658-A 6 03-NOV-1998;
Location/Qualifiers
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Gryaznov,S.M. and Lloyd,D.H.
Oligonucleoride clamps having diagnostic applications
Patent: US 5473060-A 6 05-DEC-1995;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      Unknown
{\tt Gryaznov, S.M.} Convergent synthesis of branched and multiply connected macromomolecular structures
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Sequence 6 from patent US
AR051238
AR051238.1 GI:5974602
                                  Unclassified.
1 (bases 1 to 16)
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I28367
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/mol_type="unassigned DNA"
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AR231294/c
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Search completed: March 31, Job time : 1 secs
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Sequence 31 from patent US 6451968.
AR231294
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Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
Coull,J.M., Kiely,J. and Griffith,M.
Peptide nucleic acids
Patent: US 6451968-A 31 17-SEP-2002;
Location/Qualifiers
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Similarity 90.9%;
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/mol_type="unassigned DNA"
                                                                                                                                                               organism="unknown"
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83.3%; Pred. No. 31;
tive 0; Mismatches
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AR371265
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Local Similarity 84.6%;
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149619
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Ecker, D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and
Mollegaard,N.E.
Cleaving double-stranded DNA with peptide nucleic acids
Patent: US 5641625-A 34 24-JUN-1997;
Location/Qualifiers
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                                                   AR371265
Sequence 1 from patent US
AR371265
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Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
Use of nucleic acid analogues in diagnostics and a
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Sequence 21 from patent US
AR200478
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Patent: US 6357163-A 21 19-MAR-2002;
          Unknown
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/mol_type="unassigned DNA"
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                                           GI:34608197
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AR002257/c
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Buchardt,O., Egholm,M., Nielsen,P.E. and
Peptide nucleic acids
Patent: US 6395474-A 1 28-MAY-2002;
Location/Qualifiers
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Gryaznov,S.M. and Lloyd,D.H.
Oligonucleotide clamps
Patent: US 5741643-A 6 21-APR-1998;
Location/Qualifiers
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Gryaznov,S.M. and Lloyd,D.H.
Oligonuclectide clamps having diagnostic
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Sequence 6 from patent US
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Similarity 84.6%;
                                                                                                                 Patent: US 5817795-A 6 06-OCT-1998;
Location/Qualifiers
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larity 90.9%;
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/mol_type="genomic
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0; Mismatches
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Pred. No. 2
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                                        Score 9.4; DB Pred. No. 27; 0; Mismatches
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US 5741643.
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Peptide nucleic acids complexes of two
and one nucleic acid strand
Patent: US 5986053-A 34 16-NOV-1999;
Location/Qualifiers
Higher-order structure and binding of peptide nucleic acid Patent: JP 199236396-A 8 31-AUG-1999; ISIS PHARMACEUTICALS INC, BUCHARDT DORUTE, EGUHORUMU MICHAEL, IELSEN PATER A, BERGH RORUFU HO

OS Unidentified PN 199236396-A/8 PD 31-AUG-1999 JF 199236396-A/8 PD 31-AUG-1999 JF 14-OCT-1998 JF 1998291590 PF 14-OCT-1998 US 088658 PR 02-JUL-1993 US 088658 PR 02-JUL-1993 US 088658 PR 02-JUL-1993 US 088658 PR BUSHATO ORB, EGUHORUMU MICHAEL, NIELSEN PATER A, BERG RORUFU HO, PI EKKA DAVID JAK, MORUGADO NILUS A PC CO7H21/04, A61K31/00, A61K31/00, A61K31/70, A61K48/00,
                                                                                                                                                                                                                                                                                                                                                                                            11;
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Norden, B., Wittung, P., Buchardt, O., Egholm, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ecker, D.J.,
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Bushato,O., Eguhorumu,M., Nielsen,P.A., Berg,R.H.,
                                                                                                                                                                                                      unidentified
                                                                                                                                                                                                                    unidentified
                                                                                                                                                                                                                               E36063.1 GI:13022465
JP 1999236396-A/8.
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Higher-order structure
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nilarity 84.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="unknown"
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Pred. No. 25;
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de nucleic acid.
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Local Similarity 84.6%;
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Sequence 16 from patent US 5629152.
I42181
I42181.1 GI:2467676
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                                                                                                                                                                                 Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trisubstituted .beta.-lactams and oligo .beta.-lactamamides Patent: US 5629152-A 16 13-MAY-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unknown.
                                                                                                                   Trisubstituted .beta.-lactams and oligo Patent: US 5629152-A 25 13-MAY-1997;
                                                                                                                                           1 (bases 1 to 16)
Ravikumar, V.
                                                                                                                                                                                            Unknown.
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Ravikumar, V.
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C12N15/09,C12Q1/68,C12N15/00
Strandedness: Single;
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                  Conservative
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
/mol_type="unassigned
                                                                                                     Location/Qualifiers
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                                                                 /organism="unknown"
/mol_type="unassigned DNA"
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PAT 07-0CT-1997

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Sequence 21 from patent US
AR200478
 AR231294 1
Sequence 31 from patent US
AR231294
AR231294.1 GI:27272225
                                                                                                                                            1.9%; Score 14.4; DB 1;
Similarity 93.8%; Pred. No. 4.3;
15; Conservative 0; Mismatches 1;
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Buchardt,O., Egholm,M., Nielsen,P.B. and
Peptide nucleic acids
Patent: US 6395474 A 1 28-MAY-2002;
Location/Qualifiers
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AR371265
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Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
Use of nucleic acid analogues in diagnostics and a
                                                                                                                                                                                                                                                                                               Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent: US 6357163-A 21 19-MAR-2002;
Location/Qualifiers
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larity 93.8%; Pred. No. 4.3;
Conservative 0; Mismatches 1;
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/mol_type="genomic DNA"
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Best Local Similarity 84.6%;
Matches 11; Conservative
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Other publication AU 432353 940104
Other publication AU 432353 940104
Other publication AC 2136831 931223
Other publication SK 149394 960110
Other publication HU 71931 960228
Other publication FI 945725 941205
Other publication NO 944655 950203
Other publication NO 944651 960227.
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Egholm, N. Nielsen, P., Buchardt, O., 1

Coull, J.M., Kiely, J. and Griffith, M.

Peptide nucleic acids

Patent: US 6451968-A 31 17-SEP-2002;

Coation/Qualifiers

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A36563.1
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Sequence 3 from Patent WO9325706.
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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/mol_type="genomic
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1 (bases 1 to 16)

1 (bases 1 to 16)

1 (pases 1 to 16)

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Convergent synthesis of branched and multiply connected macromomolecular structures
Patent: US 5571677-A 6 05-NOV-1996;
Location/Qualifiers
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Sequence 6 from patent US 5571677.
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/mol_type="unassigned DNA"
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/mol_type="genomic DNA"
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/mol_type="unassigned DNA"
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142181
142181.1 GI:2467676
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Ravikumar, V.
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Location/Qualifiers
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                               Cleaving double-stranded DNA with peptide nucleic acids Patent: US 5641625-A 34 24-JUN-1997; Location/Qualifiers
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Ecker, D.J., Buchardt, O., Egholm, M., Nielsen, P.E., Berg, R.H. and Mollegaard, N.E.
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_type="unassigned DNA"
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Pred. No. 4.3;
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Sequence 34
AR087164
AR087164.1
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                                                                   1 (bases 1 to 16)
Ecker, D.J., Buchardt, O.,
Mollegaard, N.E.
                                                                                                                                                                                                                                                \mathbf{L}
                                                                                                                                                                                                                                                                                                                                                                           Convergent synthesis of branched and macromolecular structures
Patent: US 5830658-A 6 03-NOV-1998;
Location/Qualifiers
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Gryaznov, S.M. and Lloyd, D.H.
Oligonucleotide clamps having diagnostic and therapeutic
                                  Peptide nucleic acids complexes of two peptide nucleic acid and one nucleic acid strand Patent: US 5986053-A 34 16-NOV-1999;
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Gryaznov, S.M.
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AR051238
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Location/Qualifiers
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Similarity 93.8%;
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34 from patent US 5986053.
                      Location/Qualifiers
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/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
/organism="unknown"
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Pred. No. 4.3;
0; Mismatches 1,
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E36063/c
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AR150597/c
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Matches 15
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Best Local Similarity 93.8%;
Matches 15; Conservative
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Patent: US 6228982-A 9 08-MAY-2001;
Location/Qualifiers
1. .16
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Sequence 9 from patent US
AR150597
AR150597.1 GI:15115188
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Higher-order structure and binding of peptide nucleic acid
E36063
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Higher-order structure and binding of peptide nucleic acid Patent: JP 1999236396-A 8 31-AUG-1999; ISIS PHARMACEUTICALS INC, BUCHARDT DORUTE, EGUHORUMU MICHAEL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 16)
Bushato,O., Eguhorumu,M., Nielsen,P.A., Berg,R.H.,
Morugado,N.A.
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JP 1999236396-A/8.
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Norden, B., Wittung, P.,
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Unidentified
JP 1999236396-A/8
31-AUG-1999
14-OCT-1998 JP 1998291590
02-JUL-1993 US
088658
02-JUL-1993 US
BUSHATO ORE, EGUHORUMU MICHAEL, NIELSEN PATER A, BERG RORUFU EKKA DAVUD JAY, MORUGADO NILUS A
COTHZ1/04, A61K31/00, A61K31/00, A61K31/70, A61K48/0
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/ \verb|crganism='Unidentified'|.\\ Location/Qualifiers
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Pred. No. 4.3;
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16 bp Sequence 3 from Patent WO9325706. A36563.1 GI:2293876

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05-MAR-1997

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Maximum Match 100%
Listing first 50 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                    2rge.db:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyright
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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AR002257
AR045207
AR051238
AR087164
AR150597
                        I49619
AR200478
AR371265
AR002257
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AR045207
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AR087164
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I42181
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ACCESSION: AR087164
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ACCESSION: I49619
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ACCESSION: AR200478

ACCESSION: AR371265

ACCESSION: AR002257

ACCESSION: AR045207

ACCESSION: AR051238
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ACCESSION: I28367
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ACCESSION: AR002257
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ALIGNMENTS

0

RESULT 1
A36563/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM RESULT 2
AR002257
LOCUS
DEFINITION
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LOCUS
DEFINITION REFERENCE AUTHORS TITLE REFERENCE AUTHORS TITLE JOURNAL FEATURES 밁 Ś 밁 Ş FEATURES COMMENT Query Match Best Local S Matches 15 Query Match Best Local Matches JOURNAL source Unclear to 1. (Dases 1 to 1.)

1 (Dases 1 to 1.)

Gryaznov, S. M. and Lloyd, J.....

Oligonucleotide clamps
Oligonucleotide clamps
Location/Qualifiers
Location/Qualifiers
1 16
"""known" 1 NA" Other publication CZ 9402951 950913
Other publication AU 4323593 940104
Other publication CA 2136831 931223
Other publication SK 149394 960110
Other publication HU 71931 960228
Other publication FI 945725 941205
Other publication NO 944655 950203
Other publication JP 8501681T 960227. 459 715 CTTTTTTTTTTGATC 730 16 AR002257 Sequence 6 1 AR002257 AR002257.1 ch 1.9%; Score 14.4; DB 1; l Similarity 93.8%; Pred. No. 4.3; 15; Conservative 0; Mismatches 1; 15, H 1 (bases 1 to 16)
Buchardt,O., Egholm,M., Nielsen,P.E.,
USE OF NUCLEIC ACID ANALOGUES IN THE 1
AMPLIFICATION Sequence 6 from patent US Unknown unidentified AR045207 Unknown. BUCHARDT OLE (DK) Patent: WO 9325706-A 3 23-DEC-1993; unclassified. 1.9%; Score 14.4; DB 1; Similarity 93.8%; Pred. No. 4.3; ACTTTTTTTTTTTTT 16 ACTTTTTTTTTTTT 474 CTTTTTTTTTTGGATC 1 Conservative /organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644" /organism="unknown" /mol_type="unassigned DNA" Location/Qualifiers from patent US GI:3963811 0; 0, Mismatches 16 bp 5 5817795. 16 bp 5741643. DNA NHIBITION <u>_</u> Length Length 16; Indels linear Indels linear and Stanley, C.J. OF NUCLEIC ACID 16; PAT PAT 29-SEP-1999 0 0 04-DEC-1998 Gaps

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The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonucleotides can be selected to specifically bind to pathogenic double-stranded DNA including specific sequences required by pathogenic bacteria or viruses for replication or virulence required by pathogenic bacteria or viruses for
                                                                                                        replication or virulence, reducing their pathogenicity. Alternatively, the oligonucleotide can be chosen to target a unique sequence of the pathogen which is not found in the genome of pathogen's host. The oligonucleotides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancerous cells containing the activated oncogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents an oligonucleotide used in the methods of the present invention
Sequence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;
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В Search completed: March 31, 2004, 14:06:04 Job time : 0.001 secs Query Match 1.2%; Best Local Similarity 76.9%; Matches 10; Conservative 255 AGGCAAAGGGAAA 267 15 AGAGAAAGAGAAA 3 0 Score 8.2; Pred. No. 0; Mismatches DB 1; Length 15; 3; Indels 0 Gaps

WPI; 2002-536030/57.

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RESULT 3
AAH20313/c
ID AAH20313;
XX
AC AAH20313;
XX
DT 31-UUL-2001 (first entry)
XX
DE DNA-EDTA-FE(II) probe; DNA cleavag
XX
CS Synthetic.
XX
FH Key
FT modified_base / **tag= b
FT / mod_base= OTHER
FT Y
XX
PN US2001002314-A1.
XX
PR 04-AUG-1998; 98US-00128732.
XX
PR 30-OCT-1987; 87US-00115922.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonuclectide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to control gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel
                                                                                                                                                                                                                                                                                                                                             Hybridisation probe; DNA cleavage; double-helix; oncogene; ss
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/note= "Thymidine has
2-5"
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sequence within a large double-helical nucleic acid. The probe is complementary to the target sequence and contains at least one nucleotide with an attached molecule that is able to cleave double-helical DNA e.g. CC EDTA-Fe(II) (ethylenediaminetetraacetic acid-iron complex). The probes where the attached molecule is a label or compound that alters gene campression, are used for specific detection and/or cleaves of double-helical DNA, e.g. for diagnosis, for treatment of disease (particularly CC caused by viruses, genetic defects or oncogenes), for chromosomal CC canalysis, and for the isolation and mapping of genes. The present consideration show it binds to and cleaves a double stranded fragment of illustrating how it binds to and cleaves a double stranded fragment of plasmid pDMAGIO given in AAH20315
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Matches 10
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12-NOV-1993;
                                                                                                                                                                                                                                                              Triple-helix formation; purine-rich target sequence; double-helix Dy gene expression; regulatory sequence; pathogenic double-stranded DN pathogenic bacteria; virus; replication; virulence; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
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                                                                                                                         17-SEP-1992;
                                                                                                                                                                               11-JUN-2002
                                                                                                                                                                                                         US6403302-B1
                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                  Triple helix forming associated oligonucleotide
                                                                                                                                                                                                                                                                                                                                                              07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                   ABK98147 standard;
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Pred. No. 0;
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A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonucleotide which binds in parallel and antiparallel orientation,

WPI; 2002-536030/57.

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Result
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Maximum Match 100%
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 31-MAY-2001.
                      US2001002314-A1.
                                                                                                                         Synthetic
                                                                                                                                             Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
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length: 2000000000
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C-5"
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                                                      "Thymidine has EDTA-FE(II) covalently attached
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DNA-EDTA-FE(II) pr
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16-NOV-1990;
12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to hybridisation probes which target a specific sequence within a large double-helical nucleic acid. The probe is complementary to the target sequence and contains at least one nucleotide with an attached molecule that is able to cleave double-helical DNA e.g. EDTA-Fe(II) (ethylenediaminetetraacetic acid-iron complex). The probes where the attached molecule is a label or compound that alters gene expression, are used for specific detection and/or cleavage of double-helical DNA, e.g. for diagnosis, for treatment of disease (particularly caused by viruses, genetic defects or oncogenes), for chromosomal analysis, and for the isolation and mapping of genes. The present sequence represents probe of the invention which is used in an example illustrating how it binds to and cleaves a double stranded fragment of
                                                                                                                                                                                                                             Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New hybridization probe for specific triplex formation with large double helices, useful e.g. for site-specific diagnostic cleavage, contains attached functional residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-342909/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-AUG-1998;
                                                                      17-SEP-1992;
                                                                                                                              11-JUN-2002
                                                                                                                                                           US6403302-B1
                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                 oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
                                                                                                                                                                                                                                                                                       Triple helix forming associated oligonucleotide #30.
                                                                                                                                                                                                                                                                                                                    07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                ABK98147;
                                                                                                                                                                                                                                                                                                                                                                            ABK98147 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid pDMAG10 given in AAH20315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dervan PB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FLEH-) FLEHR HOHBACH TEST ALBRITTON & HERBERT
                                                                                                16-DEC-1993;
                                       (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              550 TTTTCTCTTTCTCT 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 100.
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Fig 4B; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTTCTCTTTCTCT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moser HE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87US-00115922.
90US-00614205.
93US-00152250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00128732
                                                                     92US-00946976
                                                                                                  93US-00168920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; **
                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Dervan PB,

Beal PA;

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Initial Score = Residue Identity = Gaos = -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30. US-09-477-082-2 (1-753)
US-09-477-082-18 Sequence 18, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Initial Score = Residue Identity = Gaps = `
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29. US-09-477-082-2 (1-753)
US-09-477-082-34 Sequence 34, Application US/09477082
                                                                                                                                                                                                                                                                                                                        31. US-09-477-082-2 (1-753)
US-09-477-082-22 Sequence 22, Application US/09477082
× ດ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 310 320 330 X 350 X CTCTCTGAGCCGATGCCTTTGACTTTGCTACTTTTTCACTCTGAGCAGTTCCCAGTTCCTGCTACCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 270 280 290 300 CACCTCTGGTGTGCTCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 200 210 220 230 X 240 250 X TTTGTTTCTTGACTCTAGAACAGGACTGTGGGGGTGGGGGAAGCAACTTGGATCTGCCCTTCTGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        650 660 670 680 690 AAACGTTTTCGATGTGGATTTCGCGGGAAAATTAACCTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   580 590 600 610 620 X 630 640 CTGAAGGGGTTTTCCTTTTTTTTTTTTTTTTGTTGCAAA
                                                                                                                                                                                  530 540 550 550 570 X 580 590 570 X 580 590 SANTCACGARTGCCTGAAGGGGTTTCCTTTATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                370 380 390 400 410 TGTCCTGCAAGCTTCCCTGCCGCCTCGAATGCAGATACACGGACTCCCT
                                                         600 610 620 630 TICCACCCCACCCTTTCCCCTCCCTGCCCTGTTTTTGTTGCCCAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 Optimized Score = 12
57% Matches = 12
0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.7
0 ** 7
                                                                                                                                                                                                                                           6 Optimized Score = 10
43% Matches = 10
0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 Optimized Score = 11
52% Matches = 11
0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Optimized Score = 13
Matches = 13
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 Significance = -0.26
12 Mismatches = 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 Significance = -0:25
13 Mismatches = 12
ions = 0
                                                                                                                                                                                                                                           10 Significance = -0.26
10 Mismatches = 13
ions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 Significance = -0.26
11 Mismatches = 10
ions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCATATATATCTACATTCAÁAA
X 10 20
                                                                                                                      rcccdddrrrrccccaagaada
x 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trerceretierenachaecere
x 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cererarciecarregaegee
x 10 20
```

32. US-09-477-082-2 (1-753) US-09-477-082-30 Sequence 30, Application US/09477082

```
Initial Score = 5 Optimized Score = 11 Significance = -0.27
Residue Identity = 50% Matches = 11 Mismatches = 11
Gaps = 0 Conservative Substitutions = 0
AATTAGACGCGTATTGAAAGTAAAGAACTTCTTCCTGGGAGCCTTTCCCTGCTGAGGA

CGTATATCTACATTCGAAACGA
X 10 20 X
```

80 CGTGGAGT

×a

```
Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                         Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21. US-09-477-082-2 (1-753)
US-09-477-082-21 Sequence 21, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20. US-09-477-082-2 (1-753)
US-09-477-082-25 Sequence 25, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22. US-09-477-082-2 (1-753)
US-09-477-082-28 Sequence 28, Application US/09477082
                                                                                                                                                                                                                  23. US-09-477-082-2 (1-753)
US-09-477-082-15 Sequence 15, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             620 630 640 650 850 660 670 670 X CCCTGCCCTCTGTTTTGGATTCGCCGAAAAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X 520 530 540 550 560 TGTCATTCTGTCGAATGCCCTTGAGGTGCACAGCCCCTTTCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            700 710 720 730 ACCTGCACCGTTTGCAAAATGAACTTTTTTTTTTTGATCCTGTACAC
                                                                                                                                                                                                                                                                                  240 250 260 270 280 CTTGGATCTTGAGGACACCTCTGGTGCTGGCCCAGGTCT
                                                                                                  170 180 190 200 210 X 220 230 X TTCAACAGGAAACAGGGCTGTGGGGGAAGCAA
                                                                                                                                                 9 Optimized Score = 12
54% Matches = 12
0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                           0
46
25
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
60%
0
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$0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Optimized Score = 14
Matches = 14
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                         Optimized Score = 13
Matches = 13
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Optimized Score = Matches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 Significance = -0.23
10 Mismatches = 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 Significance = -0.24
13 Mismatches = 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 Significance = -0.23
14 Mismatches = 9
                                                                                                                                                                   12 Significance = -0.24
12 Mismatches = 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAAATGTTÁGTTÁATTTÁCTA
X 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGCAGGTGGGCGGGGCTC
                                                                                                                                                                                                                                                                                                                                          GTGÁATAGTÍTÍGCÁGÁGGCGÁT
X 10 20 X
                                                    GCCTACAGGTGGGTGGAAACTC
X 10 20 X
```

```
Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial Score = 8 Optimized Score = 11
Residue Identity = 52% Matches = 11
Gaps = 0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial Score = Residue Identity = Game =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24. US-09-477-082-2 (1-753)
US-09-477-082-16 Sequence 16, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25. US-09-477-082-2 (1-753)
US-09-477-082-23 Sequence 23, Application US/09477082
                                                                                                                                      Initial Score = 8 Optimized Score = 14
Residue Identity = 66% Matches = 14
Gaps = 0 Conservative Substitutions
                                                                                                                                                                                                                                    27. US-09-477-082-2 (1-753)
US-09-477-082-17 Sequence 17, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26. US-09-477-082-2 (1-753)
US-09-477-082-20 Sequence 20, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290 290 210 220 230 X TTCTTGACTTGCTCTAGAAACAGGGCTGTGGGGGTGGGGGAAGCAACTTGGATCTGCCCTTTTTGAGACACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 130 140 150 X 170 X GGTGCCAGGAAAGGTGGCCTCTTCAACAGGAAACCACAATATT
                                                                                                                                                                                                                                                                                                                                  270 280 290 300 CTGGTGCTGCCTGGGCCCAGGTCTCCTGTGAGCCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 370 380 390 390 CCTCTGCTACCTTTTTTTCCCTCCAAGCTTCCCTGCCGCCTCGAATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X 340 TCTCCTGTGTGTGTCTCTGAGCCGATGCCTTTGACTTTTGCTACTTTTTCACTCTGAGCAGTCTCCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 200 200 210 220 230 TTTGTTTCTTGACTTGCTTAGAAACAGGGCTGTGGGGGTGGGGAAGC
                                                               60 70 80 100 X 110 120 X CCCCCTTCCCTGAGCACGTGGAGTTAGGCAGGTAGGGACTCGGAGGACTGCGATGGTGCCAGGAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 Optimized Score = 9
42% Matches = 9
0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45%
0
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Matches = 9
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 Significance = -0.24
11 Mismatches = 10
:ions = 0
                                                                                                                                                             14 Significance = -0.24
14 Mismatches = 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 Significance = -0.24
9 Mismatches = 11
ons = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 Significance = -0.24
9 Mismatches = 12
ons = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cccaaccacaaagggreatg
x 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCACAGGTÁGCÁCGGAAAÁCC
X 10 20
GATGACÁTGGTGCCTGGGÁÁC
X 10 20
                                                                                                                                                                                                                                                                                                                                                                                                              TTTGCCTTATCTGAGGAGAGA
X 10 20
```

28. US-09-477-082-2 (1-753)
US-09-477-082-32 Sequence 32,

Application US/09477082

```
Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial Score = Residue Identity =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initial Score = 13 Optimized Score = 16
Residue Identity = 80% Matches = 16
Gaps = 0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14. US-09-477-082-2 (1-753)
    US-09-477-082-31 Sequence 31, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13. US-09-477-082-2 (1-753)
US-09-477-082-13 Sequence 13, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 50 50 GGGAGCCTTTCCCACCCCTTCCCTGCTGAGCACGTGGAGACTAGGCAGGTTAGGGGACTCGGAGACTGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGACÁTÁÁTGÁÁAAAGĆAGTÁÁTAAGCTTTGTTTGAÁTTGAÁTTGCAGCTÁÁATGCÁTAGCGĆTTTCTGTGGAATGTÁT
650 660 670 680 690 700 710 720
                                                                                                                                                                                                                          US-09-477-082-2 (1-753)
US-09-477-082-19 Sequence 19, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTCAAGAAAATGGATTTAAACATATTTCCCTGTGGAGGTAAAGAACATTCTTATACATTTATCAGTTTCCT
510 520 530 540 550 560 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                720 730 740 740 750 X
GAACTTTTTTTTTTGATCCTGTACACTGGTTTTTTAACCTT
                                                                                        120 130 140 150 160 X 170 180 X GETGCCAGGAAAGGTGGCCTGTTCAACAGGAAACCACAATATT
                                                                                                                                                                                                                                                                                                     120 130 140 150 160 GGTGCCAGGAAAGGTGGCCTGTTGCCAAGGTGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAGGCGATGAAAATGCTGGTGGGATCAAAGCCTTATAGAGGCTGCATTTTTACAGGTTGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 160 170 180 190
TGCCAAGGTGGCCTCTTCAACAGGAAACCACAATATTTTTTGTTTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190
  200
                                                                                                                                                   13
63*
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 Optimized Score = 17
80% Matches = 17
0 Conservative Substitutions
                                                                                                                                               Optimized Score = 14
Matches = 14
Conservative Substitutions
210
230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 Significance = -0.21
17 Mismatches = 4
                                                                                                                                                 14 Significance = -0.21
14 Mismatches = 8
ions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 Significance = -0.21
16 Mismatches = 4
ions = 0
                                                                                                                                                                                                                                                                                                                                                               TAGGGGATTTGGAGATTGTGA
X 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGGAGCGGGTGTGGGTCG
                                    TTCAGCAAAGTACCGCAATTTC
X 10 20 X
```

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Initial Score = Residue Identity = Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17. US-09-477-082-2 (1-753)
US-09-477-082-27 Sequence 27, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16. US-09-477-082-2 (1-753)
US-09-477-082-14 Sequence 14, Application US/09477082
18. US-09-477-082-2 (1-753)
US-09-477-082-24 Sequence 24, Application US/09477082
                                                                                                                                                                                                                                                    ×G
                                                                                                                                                                                                                                                                                                                                                                                                           X 650 660 670 680 690 AAAAACAAGTTCTCTAAACGTTTTCGATGTGGATTTCGCGGAAAATTAACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     580 590 600 610 620 X 630 FOR THE TRANSPORTED 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
CGTGGAGTTAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 X 20 50 60 70 AATTAGACCGCGTGTAAAAGTAAAGTTCTTCCCTGGGAGCCTTTCCCCACCCCCTTCCCTGGCTGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTGTTTCTTGACTTGCTCTAGAAACAGGGCTGTGGGGGGTGGGGAAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATTTTGACTTAGATTATATTCT
X 10 20 X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56%
0
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0
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Matches = 15
Conservative Substitutions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 Significance = -0.21
13 Mismatches = 10
:ions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 Significance = -0.21
15 Mismatches = .9
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x 10 20
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18. US-09-477-082-2 (1-753)
US-09-477-082-24 Sequence 24, Application US/09477082

Initial Score = 11 Optimized Score = 11 Significance = -0.22
Residue Identity = 50% Matches = 11 Mismatches = 11
Gaps = 0 Conservative Substitutions = 0

ACAAGTTCTCTAAACGTTTTCGATGTGGATTCGCGGAAAATTAACCTTGCACCGGTTTGCAAAATCAACTTTT

ACAAGTTCTTAAACGTTTTCGATGTGGATTCGCGGAAAATTAACCTTGCACCCGTTTGTAAATCCAACTTTTT

GGGTTTTTTAATCCAGACTTTT

720
TTTTTTTGATCCTGTACACTGGTTTTTTAACCTT

720
TTTTTTTTGATCCTGTACACTGGTTTTTTAACCTTT

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Initial Score = Residue Identity = Gaps =
                                                                                                                         Initial Score = Residue Identity =
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US-09-477-082-6 Sequence 6, Application US/09477082
                                                                                                                                                                                          10. US-09-477-082-2 (1-753)
US-09-477-082-33 Sequence 33, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 200 210 220 230 240 250 260 TCTTGAÇTTGCCCTTCTGAGGAÇACCTC
40 50 60 70 80 90 GGGAGACTTCCCTGCTGAGCAGGTGGAGTTAGGCAGGTTAGGGGACTCGGAGACTGCGĀT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTCCTACCGAAACCCTGCAGAGGGAACCTGGTACATCCAGTCACTTTGCCAGAGGCCTGAGAGAGCGATGT
520 530 540 550 560 570 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCATCACCTCAAACGAGATATATCCCGGATGAGGCTGACTTTCTGCTGGGGATGGCCACTGTGAATAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTĠAĠGAĠAGAĀĠĊAGCAĠCĊŤTGAAGĠAĀĠŤCCTĠAŤGAAŤTTTĊAĀĀŤĊTTĀAŤŤŤAĊŤĀTCŤĠGŤ
100 110 120 130 140 150
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                                                                                                                                                                                                                                                                                                                                                          ACCTGCATGTGTTCTCCCTTCAGCCTTCTACTACGACATGCACATCTTAACGTGCCTGCTCTACT
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                                                                                                   21 Optimized Score = 100% Matches = 0 Conservative Substi
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Matches = 86
Conservative Substitutions
                                                                                         Matches = 21
Conservative Substitutions
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86 Mismatches = 140
ions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    380
                                                                                                                           21 Significance = -0.15
21 Mismatches = 0
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X 10 20
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Initial Score = Residue Identity =
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US-09-477-082-8 Sequence 8, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11. US-09-477-082-2 (1-753)
US-09-477-082-29 Sequence 29, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ĆTĠŦĊŦĠAŦĊAŦĊĊAACAĀŦŢŦĠCAAAAGCĀĊGGGAGAĀAGTGCCĆĀAAĊŦŢCAĆĀĠCAŢTAGĠG
290 300 310 320 330 340 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGCCAGGAAAGGGTGGAGCGGGTGAGTGCCTGTTGCCAAGGTGGCCT
AGAAAATCCTTCTTATGCCTATTTTTTTTAAATCAAAAGGGATTTAACATAGCTATACCAAAAGGGCCATG
440 450 460 470 480 490 500
                                                                                                                                                                                                                                                                                                                                            ĠĊŤĊĊŢĠĠĠŢŤĠĠĠŢŦŢŢĠŢĄĄŤĊĊĄĠĄĊŢŢŢĠĠĊĄĄĄĞŢŢŢĀĊĊĄĄĄŢĠĄĄĄĄĠĊĄĄĄĊĊŢĊĠĠĠĠĄŢĄ
220 230 240 250 260 270 280
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150 160 170 180 190 200
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80 90 100 110 120 130 140
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X 10 20 30 40 50 60 70
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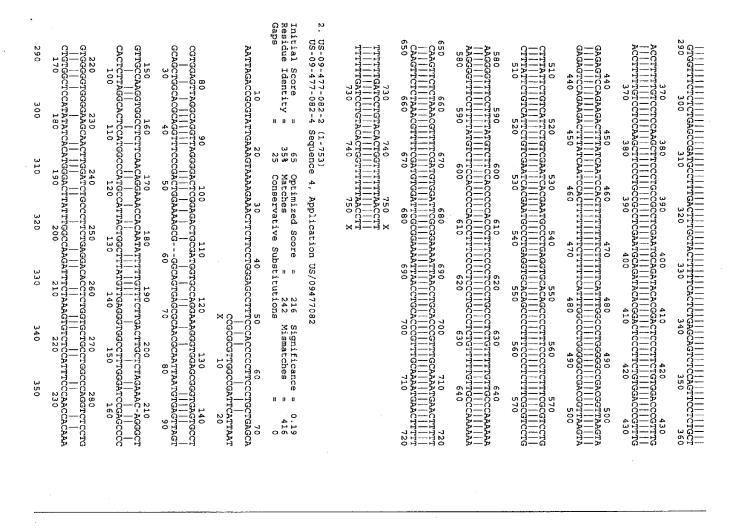
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 300 310 320 330 CTGTGTGGGTTTCTCTGAGCCGATGCCT----TTGACTTTGCTACTTTTTCACTCTGAGCAGTCTCCAGT
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33% Matches = 252 Mismatches = 501
9 Conservative Substitutions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Optimized Score = 19
Matches = 19
Conservative Substitutions
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19 Mismatches = 2
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X 10 20
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Initial Score =
Residue Identity =
                                                                                                                                                                                                                Initial Score = Residue Identity = =
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US-09-477-082-10 Sequence 10, Application US/09477082
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US-09-477-082-5 Sequence 5, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460 470 480 490 500 500 Aprovantoraria de constante de co
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100 110 120 130 140 150 160
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240 250 260 270 280 290
                                                                      370 420 430 TGTCCTCCAAGCTCCGAATGCAGATACACGGACTCCCTTCTGTGGACCCGTTTGGAGAGTC
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0 320 330 340 350 360 370 380
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                                                                                                                                                                                                                    Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGACTGGGTGACATCTGACA
                                                                                                                                                                                                                    Significance = -0.08
Mismatches = 134
0
CTTCGTGGTCTGTCTCTGGGCC
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264
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Initial Score =
Residue Identity =
Gaps =
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US-09-477-082-9 Sequence 9, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440 450 450 450 470 480 490 490 CAGAAGACTTTATCTTTTTCATTTGGCCCTGGGGGCCGACGGTT----AAGTACTT
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. 170 180 190 200 210 220 X
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100 110 120 130 140 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cochedececherretecerectereceteaetes cochedecents de cochedece de coche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCCATGGÁGACAÁGGGCATCATCTATGAGCÁCTGATGGAGC----ÁGGAGCCCCCCCATCTATGAGCTGACAT
240 250 260 270 280 290 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCTATGÁ-CÁTTTTGAÁAAATCTACCAACTCATGGÁCCACAGTAACATGGACTGCTTCATCTGCTGATCTCT
170 180 190 200 210 220
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                                                                                                                                                                                                                                                                                                                           CTCAGTTCACTGGTTTGAAGTGCCCTTCCCTTGCTGGAAAACCCAAAGTGTTTTTTTATTCAGGATTGTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 380 390 400 410 420 420 TTTGTCCTCCAAGCCCTCTCTGTGGACACGCTTTGGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGÓGCTTTGAĆCAĆGÁCTTTGÁÁGAGCTTCÁTTTTGAGATCAAGCCCCAĆGATGACTGCÁCAGTAGAGCAA
100 110 120 130 140 150 160
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30 40 50 60 70 80
                                                                                                                                                          440
TCCAGAAGACTTTATCAATCCACTTTTTTTTTTTTCATTTGCCCCTGGGGGCGACGGTTAAGTACTTTA
-- GGĠġŢŊĄĊŢĄCCAĠĄĄĄGGŢĄŢĄCCTGŢŢĠĄGACTĠĄŢŢĊĄĠĄGGAĠCĄĄCCCŢĄŢŢŢŊĠĄĄATGGAŢŢŢ
380 390 400 410 420 430
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15
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Matches = 260
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTCCTTTGCTTGTCTCTCGGT
X 10 20
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Initial Score = Residue Identity = Gaps = =
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US-09-477-082-3 Sequence 3, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            580 590 600 610 620 630 FOR TRANSCREPT TO THE TOTAL CONTROL OF THE TOTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGCAAGAATGGCATATTACTTGCCGCCGACAGGGGTTATTATTACTAAATGGAGTCAGTATAAATGC 290 300 310 320 330 340 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CÁTGGGGGTTAAATÁÁAGCGCTTT
650 660 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650 X 680 X 680 AAACAAGTTCTCTAAACGTTTCGATGTGGATTCGCGGAAAATTAACCTGCACCCGTTTGCAAAATGAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTCCAATAAAGCATGTCCAGGGCTCGGGCTTTAGTTTGCACGTCCATGAATTGTCTGCCACATCCCTCTTC
60 370 380 390 400 410 420 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 60 70 80 90 100 110
GCCTTTCCCACCCCTTCCCTGCTGAGCACGTGGAGTTAGGGAGGTTAGGGGACTCGGAGACTGCGATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCACCGCGCCCAGCCCATTGGCTTGTTTTGTÅTGTCTAĆCTTCCTAAACÅGTÅÅGÅGGGÅACTTGTCTGGTGT
230 240 250 260 270 280 290 GAAGCAACTTGGATCTTGAGGACACCTCTGGTGCTTGCCTGGCCCAGGTCTCCTGTGGTTTCTC
                                                                                                                                               TTAAAAAGATGGACTTCAGGAGAAATCTTATGATATTGGGGGAACAACTGGACAGTGAAGATCTGGCCTCCCC 220 230 240 250 260 270 280
                                                                                                                                                                                                                                                                         TĊTŤŤŤTTTCTČTČĆŤGTGĊTĠACAGCACAATĠACCAGTACĆTAGTAGTTĞCAGTAĞCCTTTĞATĠAACAAĞ
80 90 100 110 120 130
                                                                                                                                                                                                                                                                                                                                                                                                                                   35 Optimized Score = 236
36% Matches = 305
84 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X 10 20 30 40 AATTAGACÇGCGTATTGAAAGTAAAGAAACTTCTTCCTGGGA
                                                   260
                                                   270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 Significance = -0.04
305 Mismatches = 448
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Initial Score = Residue Identity = Care
                                                                                                                                                                                                                                                                                             5. US-09-477-082-2 (1-753)
US-09-477-082-7 Sequence 7, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAGGGGTCAAATTTCTGCCTACAGGTGGGTGGGAAACTCCCATTGTGGGAACTGGGAAGGTGTGGGAATGG
510 520 530 540 550 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAĞACYCCAĞAAAAGAĞAATGTTGGAĞGAAAGĆAATCTĞTCCTTCCTGAAĞGAGCTGCTCTTCCGAATTA
370 380 390 400 410 420 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGÁTGTCCCÁCCGAAGCCAGATTAAGÁÁÁTTTÁGGGGCCTTATTATATATTATÁGAAATGCTAAGÁCC
800 810 820 830 840 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440 450 500 470 480 490 490 490 AGAGICCACHTTITTTTTTTTTTATTTGGCCTTGGGGGCCGACGGTTAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAGAĊTGĠĀŤŤTGĊŤĠATTACĊTĀĊCTĀAAĊĀCTAGAĀAĠĠĀGGAGĀŤGGAĀĀĠĠGAĀĊTŤCĀĠĀCACCĀĠ
440 450 460 470 480 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        00 310 350 360 TTTGAGCTTTTTCACTATTTCACTGAGCAGTCTCCAGTTCCTCTGCTACCTTTTTG
                                                   ATAAAATAAAATTT
X 870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTCTAAAGCTTCTACAGAAGACAGTAGTGCCCTTGGTGGTCCTGCTAAAGGCTGTAAAACTTAGCTTCTCCCC
50 660 670 680 690 700 710 720
                 TTCCCGGGTTTTCCCGAGGGGGGAGGAGTTGTGTGGGGTAATGACAATCTCGGACTCTCCAAGAGAACACAGGAT
                                                                                                                                                                 31 Optimized Score = 39% Matches =
                                                                                                                                                                                                                        Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                710
60
                                                                                                                                                                                                                                          64 Significance = -0.07
69 Mismatches = 102
                                                                                                                                                                                       580
                                                                                                                                CGGGTCACCCTTGGGGTAAATT
```



Initial Score = Residue Identity = Gaps = 360 370 420 430 TACCTTTTTGTCTCCAAGCTTCCCTGCCCCCTCGAATGCAATACACGGACTCCCTTCTGTGGACCCGTTT US-09-477-082-2 (1-753)
US-09-477-082-1 Sequence 1, Application US/09477082 ÁAGCGCTCCAAGACACGÁITGCÁGAAGGAAC-ACGGGGTGGCCAACTGAAATTTGAAGAACAGGGCCAAGGA X 10 20 30 40 50 60 70 ÁGÁCCATRARATRÁAAATTT--ÄTTTTTCAAAGTGAÁACATTACTTAGAGGTATGCTGAAGTTATAATAGAG 180 590 600 610 620 630 640 CCÁCAATTÉTAÁGCTTCTACAGÁÁAAGÁÁAGTAGTGCCTTGGGTGGCCTGCTAAAAGGCTGTAAAACTTAGGT 370 380 390 400 410 420 430 TGTGGTTTCTCTCTGAGCCGATGCCTTTGACTTTGCTACTTTTTCACTCTGAGCAGTCTCCAGTTCCTCTGC GAGAAGGCTGGTCTGTGACTTCAGTGCTGAGGGTTGATCAAGGCAAAAGGGAAACTTCCTATTCCCAGACCCT 250 250 270 280 TCCTTTTTTTCTGAACGATCTACCCGCATTTCA-GCCACAGGGCTGACTTTACCCAGTCCGGCGGGGGGAAG 150 210 210. TGTTGCCAAGGTGGCCTCTTCAACAGGAAACCACAATATTTTTTGTTTCTTGACTTGCTAGAAACAGGGCT TGGGAACTCAGCCTGAGCACGGGTTGATCCGGAGCAGGGCTAAGCCAAGTACGAATGAACCAGACCACTTCC TTTAAGTTTCTTTTGCAAGAGGAAATCTCCAAATGCAAACTGGATGATGACATGGTGCCTGGGAACAGCAGG TTTTTTTGATCCTGTACACTGGTTTTTTAACCTT 310 36 Optimized Score = 219
36% Matches = 243
5 Conservative Substitutions 320 ---ATTTCAGAAGAAGTGAGCAGATCAGAATTGAGGTCT 260 270 280 290 330 219 Significance = -0.03 243 Mismatches = 424 utions = 0 340 350

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IntelliGenetics

09477082-2vs09477082-_.res 1d 2 VS. Ž to help locate primers

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Page

Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score Number of Number of Number of SCORE STDEV SHOZHGOHS чО z n n z c z Query sequence being compared:US-09-477-082-2 (1-753)
Number of sequences searched:
32
Number of scores above cutoff:
32 Results file 09477082-2vs09477082-_.res made by spaul on Wed 31 Mar 104 14:27:27-PST Sequence Name The scores below are sorted by initial score. Significance is calculated based on initial score. FastDB - Fast Pairwise Comparison of Sequences Release 5.4 Times: Scores: Randomization group 10-* 0 Results of the initial comparison of US-09-477-082-2 (1-753) with: File : US09477082.seq identical residues:
sequences searched:
scores above cutoff: 8 4 sequence to the 167 CPU 00:00:00.00 Unitary 1 Mean 40 251 2 5.00 SEARCH STATISTICS PARAMETERS 3 3 5 query sequence was found: K-tuple Joining penalty Window size Median 13 3 418 Standard Deviation 130.74 Total Elapsed 00:00:00:00.00 Init. Opt. Length Score Score Sig. Frame 586 30 500 753

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1. US-09-477-082-2 (1-753)
US-09-477-082-2 Sequence 2, Application US/09477082

Initial Score = Residue Identity = Gaps = = 220 230 240 250 260 270 270 280 760 270 7605697657657676576776669767669767766976776977697677697769767769 GTTGCCAAGGTGGCCTCTTCAACAGGAAACCACAATATTTTTTGTTTCTTGACTTGCTCTAGAAACAGGGCTG AATTAGACCGCGTATTGAAAGTAAAAGAAACTTCTTCCTGGGAGCCTTTCCCCACCCCCTTCCCTGCTGAGCA
X 10 20 30 40 50 60 70 AAITAGACCGCGTATTGAAAGTAAAAGAAACTTCTTCCTGGGAGCCTTTCCCCACCCCCTTCCCTGACGCA 100% 20 Optimized Score = 753 Matches = 753 Conservative Substitutions Significance = Mismatches = 5.45

```
Initial Score = 6 Optimized Score = 12
Residue Identity = 48% Matches = 12
Gaps = 0 Conservative Substitutions
                                                                                                                                                                                                                      Initial Score = 5 Optimized Score = 9 Significance = -0.25 Residue Identity = 42% Matches = 9 Mismatches = 12 Gaps = 0 Conservative Substitutions = 0
                                                                                                                                                                                                                                                                                                                          32. US-09-477-082-1 (1-670)
US-09-477-082-31 Sequence 31, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Initial Score = 5 Optimized Score = 9 Significance = -0.25 Residue Identity = 45% Matches = 9 Mismatches = 11 Gaps = 0 Conservative Substitutions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31. US-09-477-082-1 (1-670)
US-09-477-082-13 Sequence 13, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30. US-09-477-082-1 (1-670)
US-09-477-082-32 Sequence 32, Application US/09477082
350 360 370 380 390 GAGTCAGTATAAATGCTTTCCAATAAAGCATGTCCAGGCGCTCTTT
                                                                                                                                              80
GGGAACTCAGCCTGAGCACGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 20 X 30 40 X 50 60 70 AGCGCTCCAAGACACGATTGCAGAAGAACACGGGTGGCAACTGAAAATTTGAAGAACAGGGCCAAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 190 200 210 220
CAGCCACAGGGCTGACTTTACCCAGTCCGGCGGGAGGAGGAGGAGGAGGGCTGGTC
||
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X 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 Significance = -0.24
12 Mismatches = 13
utions = 0
                                                                          TÄGGGGATTTGGAGÄTTGTGA
X 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCATATATATCTACATTCAAAA
X 10 20
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Initial Score = Residue Identity = Gaps =
                                                                                                                                           Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24. US-09-477-082-1 (1-670)
US-09-477-082-27 Sequence 27, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23. US-09-477-082-1 (1-670)
US-09-477-082-17 Sequence 17, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Initial Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22. US-09-477-082-1 (1-670)
US-09-477-082-29 Sequence 29, Application US/09477082
                                                                                                                                                                                                           25. US-09-477-082-1 (1-670)
US-09-477-082-25 Sequence 25, Application US/09477082
                                                                                                                                                                                                                                                                                                                                       560 570 580 590 600 610 TCTCTCGGAGACCAGATTCTGCCTTTACGCCTGGAGGGAAGTGTTTTCACAGG
                                                                                                                                                                                                                                                                                      κĤ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     490 500 510 520 530 540 550 AGTGAGTCATCTTCTGTGTGAAGTTTCTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 90 100 110 120 ACTCAGCCTGAGCCACGGTTGATCCGAGCCAGGCTAAGCCAAGTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       580 590 600 610 620 CTGCCTTTACGCTGGAGGGAAGTGTTTTCACAGGGTTCTCCTTCTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCTTTAGGAGTAAAGTTTACCCTGCAGTTCCTTCTGTGGTGAAGTTTTCTCTTTTCTCTCGGAGACCAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 290 300 310 CTATTCCCAGACCCTTTGCAAGAAAGAATGGCATATTACTTGCCGCCG
                                                                                    220
 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42%
0
                                                                                                                                           50%
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 Optimized Score = 12
50% Matches = 12
0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 Optimized Score = 8
38% Matches = 8
0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Optimized Score = 9
Matches = 9
Conservative Substitutions
                                                                                                                                       Optimized Score = 10
Matches = 10
Conservative Substitutions
 240
 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 Significance = -0.23
12 Mismatches = 12
260
                                                                                                                                           10 Significance = -0.24
10 Mismatches = 10
ions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 Significance = -0.23
9 Mismatches = 12
.ons = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 Significance = -0.23
8 Mismatches = 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAGGGGATTCGGAGATTGCGA
                                GATGCAGGTGGGCGGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                            TGTCCTCGGTAAGTTTTGCCTA
X 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGACATGGTGCCTGGGAAC
X 10 20
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Initial Score = Residue Identity =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial Score = Residue Identity = Gaps =
                                                                                                               Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                    29. US-09-477-082-1 (1-670)
US-09-477-082-14 Sequence 14, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26. US-09-477-082-1 (1-670)
US-09-477-082-34 Sequence 34, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28. US-09-477-082-1 (1-670)
US-09-477-082-21 Sequence 21, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27. US-09-477-082-1 (1-670)
US-09-477-082-30 Sequence 30, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ×н
                                                                                                                                                                                                                                                                                                                            420 430 440 450 450 CCACATCCCTCTTCTGAATGGTTGGAATTGGGCATCTCTGTTCCTTTAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                       350 x 400 410 GTCAGTATAAAGCATGTCCAGCGCTCGGGCTTTAGTTTGGACGTCCATGAATTGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500 510 520 530 540 CTCTGTTCTGTTTAGGAGTAAAGTTTACCCTGCAGTTCCTTCTGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 140 150 160 X 180 190 CGAATGAACCAGACCAGTTTCAGCCACAGAGGGCTGACTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGAGGGCTGGTCTGACTTCAGTGCTGAGGTTTGATCAAGGCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 Optimized Score = 45% Matches = 0 Conservative Substi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 Optimized Score = 8
38% Matches = 8
0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 Optimized Score = 11
47% Matches = 11
0 Conservative Substitutions
                                                                                                           Optimized Score = 8 Significance = -0.24 Matches = 8 Mismatches = 15 Conservative Substitutions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 Significance = -0.24
11 Mismatches = 12
utions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 Significance = -0.24
8 Mismatches = 13
ions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 Significance = -0.24
10 Mismatches = 12
ions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTATATCTACATTCGAAACGA
X
                                                                                                                                                                                                                                                                                                                                                                                     TCAAATGTTAGTTAATTTACTA
X 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTGTATCTGCATTCGAGGCG
X 10 20
TATTTTGACTTAGATTATATTC
X 10 20
```

```
Initial Score = 8 Optimized Score = 9
Residue Identity = 42% Matches = 9
Gaps = 0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Initial Score = 9
Residue Identity = 47%
Gaps = 0
                                                                                                                                                                   17. US-09-477-082-1 (1-670)
US-09-477-082-23 Sequence 23, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Initial Score = 9 Optimized Score = 13
Residue Identity = 59% Matches = 13
Gaps = 0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial Score = 9 Optimized Score = 10
Residue Identity = 47% Matches = 10
Gaps = 0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16. US-09-477-082-1 (1-670)
US-09-477-082-26 Sequence 26, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15. US-09-477-082-1 (1-670)
US-09-477-082-19 Sequence 19, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14. US-09-477-082-1 (1-670)
US-09-477-082-33 Sequence 33, Application US/09477082
560 570 580 590 600 \times 610 620 \times CTCTTTCTCTCGGAGACCAGATTCTGCCTTTTATCGCTGGAGGGAAGTGTTTTCACAGAGGTTCTCCTTCTTTAT
                                                                                                                                                                                                                                                                            \bowtie \circ
                                                                                                                                                                                                                                                                                                                                       X 570 580 590 600 610 CGGAGACCAGATTCTGCCTTTACGCTGGAGGGAAGTGTTTTCACACGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            500 510 520 530 540 X 550 560 GTCATCTCTGTTCTGCTTAGGAGTAAAGTTTACCCTGCAGTTCCTCTTCTGTGGTGAAGTTTTCTCTTTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 120 130 140 150 X 160 170 X AGCAGGGCTAAGCCAAGTACGAATGAACCAGATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 190 200 210 220
AGCCACAGGGCTGACTTTACCCAGTCCGGCGGGAGGAGGAGAGGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580 590 600 610 620 CTGCCTTTACGCTGGAGGGAAGTGTTTTCACAGGTTCTCCTCCTTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    640 650 660 670 GTTTTTTTCGAGCCATGGGGGTTAAATAAAGCGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTCGGAGACCAGAFTCTGCCTTTACGCTGGAGGGAAGTGFTTTCACAGGGTTCTCCCTCCTTTTATCTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Optimized Score = 11
Matches = 11
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 Significance = -0.21
13 Mismatches = 9
1tions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 Significance = -0.21
10 Mismatches = 11
1tions = 0
                                                                                       9 Significance = -0.22
9 Mismatches = 12
tions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 Significance = -0.21
11 Mismatches = 12
ions = 0
                                                                                                                                                                                                                                                                                                                                                                                                          AGTTTCACTTTTCAGGGGCTTTT
X 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCAGCAAAGTACCGCAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAGGGGACTCGGAGACTGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      riciccicirciriacaacció
x 10 20
                                                                                                                                  Initial Score =
Residue Identity =
Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                 21. US-09-477-082-1 (1-670)
US-09-477-082-16 Sequence 16, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20. US-09-477-082-1 (1-670)
US-09-477-082-22 Sequence 22, Application US/09477082
                                                 200 210 220 230 240 250 260 X
TCCGGCGGGAGGAGGAGGGCTGGTCTGTGACTTCAGTGCTGAGGTTTGATCAAGGCAAAGGGAAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X 660 670
GGGGTTAAATAAAGCGCTTT
                                                                                                                                                                                                                                                                                                                    × 0.
```

8 Optimized Score = 11 47% Matches = 11 0 Conservative Substitutions

11 Significance = -0.22 11 Mismatches = 12 tions = 0

rccceerrirccceaeegea x 10 20

7 Optimized Score = 9
45% Matches = 9
0 Conservative Substitutions

9 Significance = -0.23 9 Mismatches = 11 tions = 0

CCCAACCACAAAGGGTCATG X 10 20

```
Initial Score = Residue Identity = Gaps = =
                                                                                                                                                                                     Initial Score =
Residue Identity =
Gaps =
                                                                                                                                                                                                                                                                19. US-09-477-082-1 (1-670)
US-09-477-082-15 Sequence 15, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18. US-09-477-082-1 (1-670)
US-09-477-082-24 Sequence 24, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                        410 420 430 440 450 AATTGTCTGCCACATCCCTCTTCTGAATGGTTGGAATTGGGCATCTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340 350 360 370 380 X 390 400 X CTAAATGGAGGTCTGGGGCTTTAGTTTGGACGTCCATG
                                                                                                                ACGGGGTGGCCAACTGAAATTTGAAGAACAGGGCCAAGGATGGGAACTCAGCCTGAGCACGGGTTGATCCGG
110 120 130 140 150 AGCAGGGCTAAGCCAAGTACGAATGAACCAGACCACTTCCTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   630 640 650 660 670 CTTTTGTGTTTTTTTTCGAGCCATGGGGGTTAAATAAAGCGCTTT
                                                                                                                                                                                         50*
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 Optimized Score = 12
54% Matches = 12
0 Conservative Substitutions
                                                                                                                                                                                Optimized Score = 11 Significance = -0.22 Matches = 11 Mismatches = 11 Conservative Substitutions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 Significance = -0.22
12 Mismatches = 10
1tions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                      GGGTTTTGTAATCCAGACTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCACAGGTAGCACGGAAAACC X 10 20
                                                             GCCTACAGGTGGGAAACTC
X 10 20 X
```

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Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10. US-09-477-082-1 (1-670)
    US-09-477-082-5 Sequence 5, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AČTGTCCAAGGGGAGTGGTTTCCGTTCAACTCTAAATGTCTAG
730 X 740 750 760 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 250 300 200 250 270 280 290 300 Traggeraagaring carries ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCTCTCCCATGGAGACAAGGGCATCATCTATGGCACTGATGGACAGGAGCCCCCCCATCTATGAGCTGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCTATĠĀCATTTTĠĀĀ----ĀĀTĊTĀCCĀĀĊTCĀTĠĢĀĊĊĀCĀGTĀĀČĀTGĢĀĊTGCTTCĀTĊTĠCTGTĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0 460 470 480 490 500 510 520 ATCTCTGTTCCTGTTCCTGTTCCTGTTCTGTGTTCTGTTCCTGTTCTGTTCTTGTTCTTGTTCTTGTTCTTGTTCTTGTTCTTGTTCTTGTTCTTGTTAAGGAGTAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGGAŤAAĆTAĆCÁGÁAAĠĠŤATACCŤGTTGÁĠÁCTĠÁTŤĊÁĠAGGĀGCAAĆCCŤATTTAGAÁATGGAŤTT
380 390 400 410 420 430 440
TGGCTTCTCCTTTATCCTCTCACTTCTGTCTTTCTGGGCCAGAAAACATGGAATCGCTTCCCTAGTAGCCTG
                                                                                                                                        280 290 300 310 320 330 340 CCCAGAÇÇÇÇTTATTAÇTAAATGGAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTÁCTATCTATATTCAGAGCCTATTÁGAAAGTGCTATGTGATTTAGATCÁCATTAACAGGTCÁGÁGA
660 700 710 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÁTĆ-ATĆACCTCAAACGAGATÁTAŤĆĆCGĠÁTGAĠĠĆŤĠAĆTTTCTGĆŤGGGGATGGCCACŤĠTGAAŤAACT
450 460 470 480 490 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 320 330 340 350 350 360 370 ATTACTAAARGGAGTCAGTATAAATGCTTTCCAATAAAGCATGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     380 390 440 410 420 420 430 AGGEOTICGGGGGCTTTCTGAATGGTTGGAATTGGGC
AGGGCTCGGGCTTTAGTTTGCACGTCCATGAATTGTCTGCCACATCCCTCTTCTGAATGGTTGGAATTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  свесттватссввавсавосталвескальста сватралеса, сса стесстестте степального
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCTCGGTAAGTTTTGCCTACTCAGCCCTCCTCACTGTTACAC----TACCTTCCCCCCCCTACTCCATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
33*
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Optimized Score = Matches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches = ...
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGGÁCTGGGTGÁCATCTGÁCA
X 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       640
```

Residue Identity = Gaps =

11

10 Optimized Score =

15 Significance = -0.21 15 Mismatches = 6

00

Conservative Substitutions

71%

13. US-09-477-082-1 (1-670) US-09-477-082-18 Sequence 18, Application US/09477082

```
Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                   12. US-09-477-082-1 (1-670)
US-09-477-082-20 Sequence 20, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial Score = Residue Identity = Gaps = Figure 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11. US-09-477-082-1 (1-670)
US-09-477-082-28 Sequence 28, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 350 370 420 420 GTATAAAGCATGTCCAGGCTCGGGCTTTAGTTTGCAGGCTCCATGAATTGTCTGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAAATTAAAAAAAATCTAATCTAAAAACCAGTAGGGCTCAATCAGATTCCAACTTTATTTCTCCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCCCTCTTCTGAATGGTTGGAATTGGGCATCTCTGTTCCTTTAAACAGGAAACATTTCTTGTTCGAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGCTGTGAGAGACCAGCAGAAACTGTCAGAAACTTGGGAAGCAAGGGCAGGTCCTTG-GTTGGAGAAATT
                                                                                                                           530 540 550 560 570 X 580 590 X CCTGCAGTTCCTCTGGAAGTTTCTCTCTCTCTCGGAGAAGTTCTCTCTGGAGGGAA
                                                                                                                                                                                                                                                                                                                                                     .80 190 200 210 220 230 240 250
CACAGGGCTGACTTTACCCAGTCCGGCGGGAGGAGGAGGAGGATGGTTGTGTGACTTCAGTGCTGAGGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACCGCAATTTCCTATGTTTTAACCCAGCAGCATAGCTCAGAAGGGGGCCTTGGGCAGCTCGATAATCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TĠĄĄĄĄĠĠTCTGTGCCCĄĄĄTCĄĄCĄĠĄĠCCTGCTGĄĄGATĄATCĄĄCGĄCTATGĄĄGĄĄTTCĄGCĄĄĄG
.0 320 330 340 350 360 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTAČAACCTGCTGGATATTTTCATĀGAGATGGAGAAGĀGGGTĆATCCTGĠĠAĠAĀĀGGAAAGTTGGAĆATCC
240 250 260 270 280 290 300
11 Optimized Score = 14
66% Matches = 14
0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Optimized Score = Matches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative Substitutions
                                                                                                                                                                                                            14 Significance = -0.20
14 Mismatches = 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 Significance = -0.19
12 Mismatches = 10
                                                                                                                                                                                                                                                                                                                                                                                                                         GTGAATAGTTTGCAGAGGCGAT
X
                                                                  TTTGCCTTATCTGAGGAGAGA
X 10 20
```

```
Initial Score = 25 Optimized Score = 220
Residue Identity = 36% Matches = 247
Gaps = · 13 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-477-082-1 (1-670)
US-09-477-082-8 Sequence 8, Application US/09477082
                                                                                                                                                                                 GCAAACCTCGGGGGATACTGTCTGATCATCCAACAATCACAATTTTGCAAAAAGCACGGGAGAAAGTGCCCAAA
280 290 300 310 320 330 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u> АСВАНОБААСАСОО О ОТОВАНАТТТО В АВСЕДО В В СЕТО В В СЕТО В В СЕТО В В ЕВ В В В В ЕВ В В В В В В ЕВ В В В В В</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAACGATGGGGCAGAAGTCTGAGAGGTCCTGTGTGAAGGAAATAGGTAGAAACTAGTTCTTCGAGGAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATCCTTTTTTÄÄATTACÄTTACAGATTČTAGTTTTTTTAATTTGTTAGČT
130 140 150 160 170 X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 X 200 210 CTTTTTTTTTGAACGATCTACCCGCATTTCAGCCACAGGGCTGACTTTACCCAGTCCGGGGGAGGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGGGGTAÁTGACAÁTÓTCGGAACÍTCTCCAAGÁGAÁAÁGAGATÁGTGÁÁTCCCAAGGTAGCACGGÁAAÁÓCTCCA
60 70 80 90 100 110 120
                                                             GGGCATCTCTGTTCCTTTAAACAGGAAACATTTCTTGTTCGAGT--GAGTCATCTCTGTTCTGCTTTAGGAG
                                                                                                                             TACCAAAAGGGCCÁTGGTTCÁAGAAAAÁTGGÁTTTAAACATÁTTTCCCTGTGGAGGTAAAGAACATTCTTÁTA
.90 500 510 520 530 540 550 560
                                                                                                                                                                                                                                                                                                                      310 320 330 340 350 360 370 ACTTGCCGCCGACAGGGTATAAAGGATGTCCAATAAAGGATGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                            TTGACCCACAGAGTCAGCTCCTGGGTTTGGGTTTTTGTAATCCAGACTTTGGACAAAAGTTTACCAAATGAAAA
210 220 230 240 250 260 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 230 240
GAGGGCTGGTCTGTGACTTCAGTGCTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                440
                                                                                                                                                                                                                                                             450
                                                                                                                                                                                                                                                             460
                                                                                    490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 Significance = -0.08
247 Mismatches = 420
tions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X 10 20
AAGCGCTCCAAGACACGATTGC
```

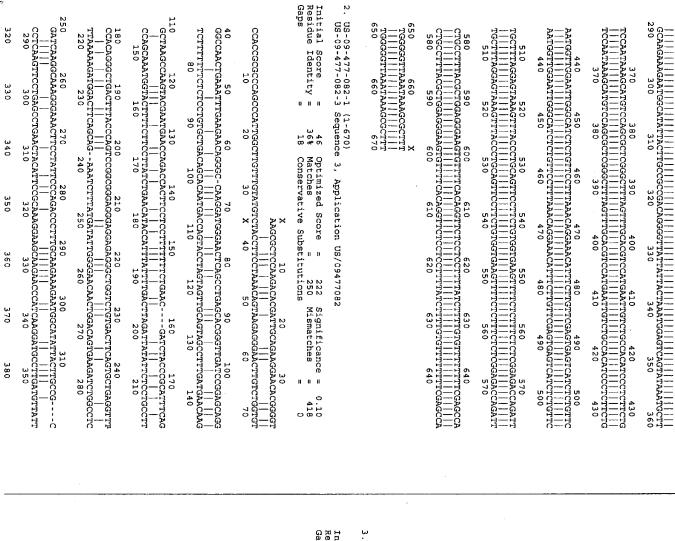
```
Initial Score = Residue Identity =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Initial Score = 24
Residue Identity = 37%
Gaps = 5
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US-09-477-082-10 Sequence 10, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                     9. US-09-477-082-1 (1-670)
US-09-477-082-9 Seguence 9, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               660 670
TAAAGCGÇTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAACAGATGCCTCAGCCTACTTTCACACTAAGAAAAAACTTGTCTTCCCTTCTGATTGA 170 180 190 200 210 220 X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATATICTCACCATCCTGACTGAAGTGAACTATGAAGTAAGCAACGAGG-----ATGACAAGAAAAAACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 280 290 300 310 X 320 330 SAAACTTCCTATTCCCAGACAGACATTAGAAAGAAAGAAATGGCATATTACTTGCCGCCGACAGGGGTTATTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTCTGTGGAATGTATTAGGCGATGAAAATGCTGGTGGGATCAAAG--CCTTATAGAGGCTGCATTTTTACA 710 720 730 740 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cregaegeaagregrificacaegricicorocritiarorritarerritirocaegocaregegeriaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAAGTTTACCCTGCAGTTCCTTCTGTGGAAGTTTTCTCTTTTCTCTGGAGACCAGATTCTGCCCTTTACG
                                                                                                                                    TGTCCTGCACTCTCCCTGCTGGTCTGTGCTTATAGTGTGGGCTÅCTGTTCGAGTTTCACTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          560 570 580 590 TTCTCTCTCGGAGACCAGATTCTGCCTTTACGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>AATTGTCTGCCACATCCCTCTTCTGAATGGTTGGAATTGGGCATCTCTGTTCCTTTAAACAGGAAACATTTC</u>
                                                                 AGAAG----GAACACGGGGTGGCCAACTGAAATTTGAAGAACAGGGCCAAGGATGGGAACTCAGCCTGAGCA
                    ÄGGGGCTTTGACCACGACTTTGAAGÄGCTTCÄTTTTGÄGÄTCAAGCCCCACGATGACTGCACÄGTAGAGCAA
110
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                                                                                                                                                                                                                                                                                Conservative Substitutions
                                                                                                                                                                                                                                                                                                       Optimized Score = Matches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130
130
140
                                                                                                                                                                                                                                                                                                       222 Significance = -0.10
255 Mismatches = 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 Significance = -0.09
86 Mismatches = 137
ions = 0
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AAGCGCŢĊĊĄAGACACGAŢŢĠÇ
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Initial Score = Residue Identity = Gaps
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US-09-477-082-4 Sequence 4, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACCTTTTTGTCCTCCAAGCTTCCCTGCCGCCTCGAATGCAGATACACGGACTCCCTTCTGTGGACCCGTTT 360 390 400 410 420 430
ACTGGATGÁTGÁCAÍGGTGÉCCTGGGAACAGCAGGCCACAATÍCTAAGCTTCTACAG--AAAAGACAGÍAGTG
330 340 350 360 370 380
                                                                                                                                                                                 290 300 310 350 360
GCAAGAAAGAATGGCATATTACTTGCCGCCGACAGGGGTTATTATTACTAAATGGAGTCAGTATAAATGGTT
                                                                                                                                                                                                                                                580 590 600 610 620 630 590 F4U FICT CCTCTTTATCTTTTGTGTTTTTTTTTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAGAGTCCAGAAGACTTTÁTĆAATCCAĆTŤŤŤTTTTTTTTTTŤÁŤŤŤGGCCCŤGGGGGCGAĆGGTŤAAĠŤ
440 450 460 470 480 490 500
                                                         370 380 390 400 410 420 420 TCCAATAAAGCATGCAGCGTCCAGCATCCCTCCTCCTG
                                                                                                                        TTCAGAAGAAGTGAGCAGATCAGAATTGAGGTCTTTTAAGTTTTCTTTTTGCAAGAGAGAAATCTCCAAATGCAA 260 270 280 290 300 310 320
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAACAAGTTCTCTAAACGTTTTCGATGTGGATTCGCGGAAAATTAACCTGCACCCGTTTGCAAAATGAACTT 650 650 700 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATGGGGGTTAAATAAAGCGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCATGCCATTACTGGCTTTATGTTGAGGGTGGCCTTTGGGATCCGAGCCCCCTGTGGGCTCCATATATCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCCCGACTGGAAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGTCACTCTTTAGGCACTCCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               АЛВСВСТСОЛАВАСАСВАТТВСАВАЛАВБАЛСАСВЕВСТВОЛАСТВАЛАТТТВАЛВАЛАСАВВЕССАЛЬВАТ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTITATICTG-TCATTCTGTCGAATCACGAATGCCCTGAGGTGACACAGCCCCTTTTCCCCTCTTTCGCGTCC 510 520 530 540 550 560 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36
36
11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Optimized Score = Matches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CÓGCGCGTTGGCCGATTCATTAATGCAG--CTGGCACGCACGTX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 Significance = -0.01
231 Mismatches = 399
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Initial Score = Residue Identity = Gaps = Figure 1 = Fi
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US-09-477-082-7 Sequence 7, Application US/09477082

    US-09-477-082-1 (1-670)
    US-09-477-082-6 Sequence 6, Application US/09477082

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGGGTTAAATAAAGCGCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 470 480 490 TGTTCCTTTAAACAGGAAACATTTCTTGTTCGAGTGAGTCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGCCGCCGACAGGGGTTATTACTAAATGGAGTCAGTATAAATGCTTTCCAATAAAGCATGTCCAGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTG----GCAAAATCGGCTACCATATCACAGGTGTTTTTAGTCAACTGTTGTTCGGGGGGTACCCTTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGCATTTCAGCCACAGGGCTGACTTTACCCAGTCCGGCGGAGGAGGAGAGGGCTGGTCTGTGACTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 590 600 590 CTGCCTTTTACCTTTTTGTGTTTTTTTTTTCGAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAGAGĀGAAACCĀCATTCĀGTATCACTTGGGAAGGCTTTGGGĀĀG-----ATGTCCCĀCCGGAGCCĀGĀTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u> АЛССССТССАЛБАСАСБАТТССАБАЛСБААСАССССССТСССАЛСТСАЛАТТТСВАЛСАССССАЛСБАТ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGTACCTGCATGTGTTCTCCCCTTCAGCCTTCTACCACACATGCACATCTTAACGTGCCTGCTCTACT
170 180 190 200 210 220 X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 Optimized Score = 80
37% Matches = 86
4 Conservative Substitutions
                                                                                                                                                                                                                                                                                                        3525
0#5
CGGGTCACCCTTGGGGTAAATTTTCCCCGGGTTTTCCCCGAGGGGAGGAGGTTGT
X 10 20 30 40 50
                                                                                                                                                                                                                                                                                             Optimized Score = 62
Matches = 62
Conservative Substitutions
                                                                                                                                                                                                                                                                                                  62 Significance = -0.08
62 Mismatches = 115
ions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Significance = -0.03
Mismatches = 142
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X 10 20
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Initial Score = 36 Residue Identity = 36% Gaps = 5 3. US-09-477-082-1 (1-670) US-09-477-082-2 Sequence 2, Application US/09477082 390 400 450 450 FTAGTTTGCACATGAATGCCTCTTCTGAATGGTTGGAATTGGGCATCTCTGTTCCT CCCACCCTAGAGAGTGGGTAAACAAAGGCGTGAGAGAGAAACCAACAT
720 730 740 750 760 390 410 420 430
TTTCCAATAAAGCATGTCCAGCGCTCGGGCTTTAGTTTGCACGTCCATGAATTGTCTGCCACATCCCTTCTTC 150 170 200 210 CONTITUTE TOTAL CARROLL AND A CARROLL AND CGTGGAGTTAGGCAG-GTTAGGGGACTCGGAAGACTGCGATGGTGCCAGGAAAAGGGTGGAGCGGGTGAGTGCC 80 90 100 110 120 130 140 CARTTCTÁAAGCTTCTACAGAAGACÁGTAGTGCCTTGGTGGTCCTGCTAAAGGCTGTAAAACTTAGCTTCTC 650 660 700 710 X GGACAGCCTCTGAGCTGATTGGGGCTTTTTTTTTGTGGTACCCTGGCTAGTGCCTGGGAACCCAGCAGTGCCA 580 590 600 610 620 630 ĆCĀGĀĠĀCYCCĀGGĀĀĀĀGĀGĀTĠTTĠGĀGGĀĀAGCĀĀTĊTGTCCTTGAAGGĀGGĀGCTGCTCTTCCGĀAT 160 370 380 390 400 410 420 430 GTGGGGGTGGGGAAGCAACTTGGATCTGCCTTTGAGGACACCTCTGGTGCTGGCCCCAGGTCTCCTG TGGGAACTCAGCCTGAGCAGGGTTGATCCGGAGCAGGCTAAGGCAAGTACGAATCAGCAACCACTTCC AGGCAGGGCTCAAATTTCTGCCTACAGGTGGGAAACTCCCATTGTGGGAACTGGGAAGTGTGGGTTGAAT 510 520 530 540 550 560 570 470 480 500 510 520 TIDARCAGGRACATTICT ----TGTTCGAGTGAGTCATCTCTGTTCTGCTTTAGGAGTAAAGTTACC CGACAGGGGTTATTATTACTAAATGGAGTCAGTATAAATGCTTTCCAATAAAGCATGTCCAGCGCTCGGGCT TGTGGTTTCTCTCTGAGCCGATGCCTTTGACTTTTTCACTTCTGAGCAGTCTCCAGTTCCTCTGC 290 300 310 320 330 340 350 ATTAGACCGCGTATTGAAAAGTAAAAAGTTCTTCCTGGGAAGCCTTTCCCACCCCCTTCCCTGCTGAGCA X 10 20 30 40 50 60 70 х 70 г. дострои в 10 г. дострои в В 10 г. дострои в 10 г. дос TAATAGACTGGATTTGCTGATTACCTAACTATACACTAGAAAGGAGAGAGGGAGATGGAAAGGGGAACTTCAGACACC 290 300 310 320 330 CT TIGCCGCCGACAGGGGTTATTATTACTAAATGGAGTCAGTATAAATGC Optimized Score = 219
Matches = 243
Conservative Substitutions 219 Significance = 0.02 243 Mismatches = 424 tions = 0

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Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
                                                                                                                                                                                                                                                                                                                                                                                         SECPEROES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Name
                                A 100% identical sequence to the query sequence was found:
                                                       The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                   Number of residues:
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     чO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M M M K C K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query sequence being compared:US-09-477-082-1 (1-670)
Number of sequences searched: 32
Number of scores above cutoff: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Results file 09477082-1vs09477082-_.res made by spaul on Wed 31 Mar 104 14:25:38-PST.
                                                                                                                                                             Times:
                                                                                                                                                                                             Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FastDB - Fast Pairwise Comparison of Sequences Release 5.4\,
                                                                                                                                                                                                                                        Randomization group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Results of the initial comparison of US-09-477-082-1 (1-670) with: File : US09477082.seg
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  Description
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                                                                                                                                                                                                                                                                          K-tuple
Joining penalty
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32
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                                                                                                                                                 Total Elapsed 00:00:00:00.00
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Init. Opt.
Length Score Score Sig. Frame
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000000000000000000000000000000000000000	rame	0

Initial Score = Residue Identity = Gaps = -1. US-09-477-082-1 (1-670) US-09-477-082-1 Sequence 1, Application US/09477082 670 100% 0 Optimized Score = 670 Matches = 670 Conservative Substitutions 670 670 Significance =) Mismatches = =

5.46 0

150 160 170 180 190 200 210 CTTTTTTTTTGAACGATCTACCCGCATTTCAGCCACAGGGCTGACTTTACCCACTCCGGCGGAAGGAA	100 GGGAACTCAGCCTGAGGGGTTGATCCGGAGCAGGCGAAGGCAAGTACGAATGAACCACACTTCCT	X 10 20 30 40 50 50 60 70 AAGCGCTCCAAGACACGGATTGCAGAAGGAACACGGATTGCAGACACGGATTGCAGACACGGATTGCAGACACGGATTGCAGACACGGATTGCAGACACGGATTGCAGAACACGGATTGCAGAACACGGATTGCAGAACACGGGACCAACTGAAATTTTGAAGAACACGGGCCAACGATCAGAACACGGATCCAAGACACACGATTGCAGAACACGGAACACGGACCAACTGAAATTTGAAGAACACGGGCCAACGATCAAGACACGGATGCAAGATTTGAAGAACACGGGCCAACGATGAACACGGATGCAAACACGGATGCAAACACGGATGCAAACACGGATCGAACTTGAAGAACACAGGGCCAACGATACACACAC
170 CCGCATTTCAGCCA(100 TTGATCCGGAGCA TTGATCCGGAGCA	30 AGAAGGAACACGG
0 ACAGGGCTGACTI	110 AGCAGGGCTAAGCCAAG! AGCAGGGCTAAGCCAAGGCTAAGCCAAGGGCTAAGCCAAGGCTAAGCCAAGCCAAGCCAAGCAAG	40 GGTGGCCAACTGI GGTGGCCAACTGI 40
200 TACCCAGTCCGG	130 	50 VAATTTGAAGAAC VAATTTGAAGAAC VAATTTGAAGAAC 50
210 CGGGAGGGAGGA	140 AGACCACTTCCT aGACCACTTCCT AGACCACTTCCT 140	70 AGGGCCAAGGAT AGGGCCAAGGAT 70

CCTTTTTTTCTGAACGATCTACCCAATTCAGCCACACGGCTCACCTTACCCACTCCAGCGGGGAGGA